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(54) Title: METHODS OF UTILIZING THE TT VIRUS

(57) Abstract

The present invention relates to nucleic oligomer primers or probes useful for detection of TTV in test samples. Also provided are assays which utilize these primers and probes, as well as test kits which contain these oligomer primers and/or probes. In addition, the present invention encompasses the use of TTV nucleotide sequences as nucleic acid vectors and as markers for determining transmission between individuals as well as the route thereof. Additionally, the present invention encompasses a method of detecting TTV infection prior to xenotransplantation of a tissue or organ.

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METHODS OF UTILIZING THE TT VIRUS

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention relates generally to the TT virus and to methods of use thereof. More particularly, the present invention relates to nucleic acid primers useful for detection of the TT virus, use of the TT virus as a vector, use of the TT virus for human and veterinary diagnostics, and use of the TT virus for testing prior to transplantation or xenotransplantation. Additionally, the present invention includes use of TT virus sequence diversity as a means of monitoring viral transmission between individuals.

Background of the Invention

Recently, a novel human DNA virus was isolated from the serum of a Japanese patient (initials T.T.) with cryptogenic hepatitis (Nishizawa et al., Biochem Biophys Res Commun 241:92-97 (1997)). Utilizing PCR, TT virus (TTV) was detected in sera from three of five patients with non-A to GBV-C hepatitis. Subsequently, the nearly complete nucleotide sequence of the TTV genome, encompassing 3739 bases, and a more sensitive PCR assay for the detection of virus in serum were reported (Okamoto et al., Hepatol. Res. 10:1-16 (1998)). In addition, based upon sensitivity to single-strand but not double-strand-specific endonucleases, the virus appeared to possess a single-stranded DNA genome. Data presented regarding the size of the genome, its single-strandedness, and resistance to detergents, suggested that TTV was similar to the parvoviruses (Okamoto et al., Hepatol. Res. 10:1-16

(1998)). However, the buoyant density in CsCl (1.31-1.32 g/ml) was lower than that reported for the parvoviruses.

Several PCR studies have been performed to assess the prevalence of this virus in various populations. One assay described by Okamoto et al. (Okamoto et al., Hepatol. Res. 10:1-16 (1998)) detected TTV DNA in hemophiliacs (68%), intravenous drug abusers (40%), patients on maintenance hemodialysis (46%) and those with cryptogenic hepatitis and/or chronic liver disease (46-48%). Further, TTV infection in Japanese normal blood donors was found to be 12%. The rates of TTV infection in the United Kingdom have recently been reported at 1.9% (19 of 1000 blood donors) (Simmonds et al., The Lancet 352:191-194 (1998)) using two distinct primers sets and 10% (3 of 30 healthy controls) (Naoumov et al., The Lancet 352:195-197 (1998)) using the PCR strategy of Okamoto (Okamoto et al., Hepatol. Res. 10:1-16 (1998)). Both of these reports identified TTV DNA in patients at risk for acquiring parenterally transmitted viruses (27-39%) and/or in patients with hepatitis (19-22%). These studies suggest that TTV can be transmitted via blood or blood products and may also be associated with some cases of cryptogenic hepatitis.

The preliminary epidemiological studies of TTV described above utilized several different first generation PCR primer pairs. Desai et al. (Desai et al., J. Infect. Dis. in press:(1999)) compared the sensitivities of two first generation TTV PCR primers sets and demonstrated that the majority of TTV-positive samples were detected by only one of the two primer sets. Thus, previous reports that utilized a single PCR primer pair may have significantly

underestimated the true prevalence of the virus. Second generation PCR assays for TTV appear to confirm the underestimation of TTV prevalence. Specifically, a PCR assay described by Takahashi et al (Takahashi et al., Hepatol. Res. 12:233-239 (1998)) that was 10 to 100 times more sensitive than the assay described by Okamoto et al (Okamoto et al., Hepatol. Res. 10:1-16 (1998)) found TTV present in 92 of 100 healthy individuals who visited a Japanese hospital for routine health screening. Therefore, TTV prevalence in the normal Japanese population appears to be much higher than the 12% originally reported.

The high rate of TTV carriers in the normal population may not be compatible with an exclusive parenteral transmission route. A possible fecal-oral transmission route was suggested by a study that demonstrated the presence of TTV in the feces of infected humans (Okamoto et al., J. of Med. Virol. 56:128-132 (1998)). Additional non-parenteral routes of infection may explain the high prevalence of TTV infection in healthy individuals. Finally, based upon limited prevalence studies and the high rates of TTV in the normal populations (Charlton et al., Hepatology 28:839-842 (1998; Naoumov et al., The Lancet 352:195-197 (1998; Simmonds et al., The Lancet 352:191-194 (1998)), the association between TTV infection and human hepatitis is questionable.

The detection of TTV in test samples can be enhanced by the use of DNA amplification assays that utilize DNA oligomers as primers, since the amount of DNA target nucleotides present in a test sample may be in minute amounts. Methods for amplifying and detecting a target nucleic acid sequence that may be present in a test sample are well-known in the art.

Such methods include the polymerase chain reaction (PCR) described in U.S. Patent Nos. 4,683,195 and 4,683,202, the ligase chain reaction (LCR) described in European Patent Application EP-A-320 308, gap LCR (GLCR) described in European Patent Application EP-A-439 182 and U.S. Patent No. 5,427,930 which is incorporated herein by reference, multiplex LCR described in International Patent Application No. WO 93/20227, and the like. These methods have found widespread application in the medical diagnostic field as well as in the fields of genetics, molecular biology and biochemistry.

It would be advantageous to provide DNA oligomer primers derived from TTV and diagnostics, and test kits which utilize these primers. Such primers could greatly enhance the ability to more accurately detect TTV infections, and track the virus' route of transmission.

In addition to the advantages of viral detection, viruses have the potential to serve as vectors for purposes such as expression of cloned genes in culture and development of treatments for disease through gene therapy. Viruses that have been developed into vectors include those with DNA genomes such as adeno-associated virus (see, e.g., Muzyczka, N., Current Topics in Microbiol. and Immunol. 158:97-129 (1992) and Kotin, R.M., Human Gene Therapy 5:793-801 (1994)), adenovirus (see, e.g., Haj-Ahmad et al., J. Virol. 57:264-274 (1986) and Berkner, K.L., BioTechniques 6:619-629 (1988)), herpes virus (see, e.g., Breakefield et al., New Biol. 3:203-218 (1991) and Wolfe et al., Nature Genetics 1:379-384 (1992)) and papovavirus (see, e.g., Grossi et al., Arch. Virol. 102:275-283 (1988) and Milanesi et al., Mol

Cell. Biol. 4:1551-1560 (1984)), and those with RNA genomes such as modified retroviruses (see, e.g., Gazit et al., Journal of Virology 60:19-28 (1986) and Palmer et al., Proc. Natl. Acad. Sci. USA 84:1055-1059 (1987)).

DNA viruses with small genomes, such as TTV, typically encode relatively few proteins and rely on the host cell to provide most replication and expression functions, thereby reducing the complexity of their interaction with the host cell. Furthermore, TTV infection does not appear to be associated with any disease, as is evidenced by its presence in nearly 100% of some human, normal populations. Its high prevalence also suggests that infection occurs readily, and that re-infection is common, as is implied by co-infections with multiple strains. All these traits are desirable in a gene therapy vector, which should be uncomplicated, non-pathogenic, easily delivered and have the potential for multiple treatments, or for being maintained over extended periods of time.

Comparison of numerous TTV genomes has demonstrated a high sequence diversity and an apparent lack of geographic localization. This implies either a high mutation rate, due to a low fidelity replicase, or an ancient virus family that has undergone extensive evolutionary drift. Researchers of HIV have used its sequence diversity as a basis for epidemiological studies and to demonstrate specific transmission of a viral infection from one individual to another. Likewise, the diversity of TTV may help establish the primary route of infection, and benefit investigations, such as forensics, that attempt to demonstrate contact between individuals.

All U.S. patents and publications are herein incorporated in their entirety by reference.

SUMMARY OF THE INVENTION

The present invention includes primers of probes specific for TT virus (TTV). These primers or probes are represented by SEQ ID NO:29, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70 and SEQ ID NO:71. Of particular interest within the above grouping are SEQ ID NOS:60-71.

dditionally, the present invention encompasses a method for detecting the presence of TTV target nucleotides which may be present in a test sample. This method comprises the steps of:(a) contacting a test sample suspected of containing a target TTV nucleotide sequence with a TTV primer pair consisting of: 1) SEQ ID NO:60 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71, to form a reaction mixture which generates a product; (b) contacting the reaction mixture with a TTV primer pair consisting of: 1) SEQ ID NO:62 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71, wherein the nucleotide sequence of the selected primer hybridizes with the product of the reaction mixture of (a); and (c) detecting the presence of the TTV target nucleotide in the test sample. The primer

pair of step (a) consists of, for example SEQ ID NO:60 and SEQ ID NO:61, and the primer pair of step (b) consists of for example, SEQ ID NO:62 and SEQ ID NO:63.

Furthermore, the present invention also includes a method for detecting the presence of TTV target nucleotides which may be present in a test sample comprising the steps of: (a) contacting a test sample suspected of containing a target TTV nucleotide sequence with a TTV primer pair consisting of: 1) SEQ ID NO:64 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71, to form a reaction mixture which generates a product; (b) contacting the reaction mixture with a TTV primer pair consisting of: 1) SEQ ID NO:66 and 2) a primer selected from the group consisting of SEQ ID SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71, wherein the nucleotide sequence of the selected primer hybridizes with the product of the reaction mixture of (a); and (c) detecting the presence of the TTV target nucleotide in the test sample. The primer pair of step (a) consists of, for example SEQ ID NO:64 and SEQ ID NO:65, and the primer pair of step (b) consists of, for example, SEQ ID NO:66 and SEQ ID NO:67.

Moreover, the present invention also encompasses a method for detecting the presence of TTV target nucleotides which may be present in a test sample. This method comprises the steps of: (a) contacting a test sample suspected of containing a

target TTV nucleotide sequence with a TTV primer pair consisting of: 1) SEQ ID NO:68 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO;67, SEQ ID NO:69 and SEQ ID NO:71, to form a reaction mixture which generates a product; (b) contacting the reaction mixture with a TTV primer pair consisting of: 1) SEQ ID NO:70 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71, wherein the nucleotide sequence of the selected primer hybridizes with the product of the reaction mixture; and (c) detecting the presence of the target TTV nucleotide in the test sample. The primer pair of step (a) consists of, for example, SEQ ID NO:68 and SEQ ID NO:69, and the primer pair of step (b) consists of, for example, SEQ ID NO:70 and SEQ ID NO:71. In any of the above methods, the test sample may be isolated from a human or an animal; thus, the methods may be used for both human and veterinary diagnostic purposes.

Additionally, the present invention includes a test kit for detecting target TTV nucleotides in a test sample, comprising: (a) a container containing a primer pair specific for a TTV target nucleotide, wherein said primer pair consists of 1) SEQ ID NO:60 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71; and (b) a container containing a primer pair specific for TTV, wherein said primer pair consists of 1) SEQ ID NO:62 and 2) a primer selected from the group consisting of

is SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO;69 and SEQ ID NO:71. The primer pair of (a) consists of, for example, SEQ ID NO:60 and SEQ ID NO:61, and said primer pair of (b) consists of SEQ ID NO:62 and SEQ ID NO:63.

The present invention also encompasses a test kit for detecting target TTV nucleotides in a test sample, comprising: (a) a container containing a primer pair specific for a TTV target nucleotide, wherein the primer pair consists of 1)SEQ ID NO:64 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65. SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71; (b) a container containing a primer pair specific for TTV, wherein the primer pair consists of 1) SEQ ID NO:66 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71. The primer pair of (a) consists of, for example, SEQ ID NO:64 and SEQ ID NO:65, and the primer pair of (b) consists of, for example, SEQ ID NO:66 and SEQ ID NO:67.

Additionally, the present invention includes a test kit for detecting target TTV nucleotides in a test sample, comprising: (a) a container containing a primer pair specific for a TTV target nucleotide, wherein the primer pair consists of: 1) SEQ ID NO:68 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71; (b) a container containing a primer pair specific for TTV, wherein the primer pair consists of: 1) SEQ ID NO:70 and 2) a primer selected from the group consisting of SEQ ID

NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71. The primer pair of (a) consists of, for example, SEQ ID NO:68 and SEQ ID NO:69, and the pair of (b) consists of, for example, SEQ ID NO:70 and SEQ ID NO:71. Any of the test samples may be isolated from a human or an animal.

Furthermore, the present invention also encompasses a TTV-based vector comprising: 1) a promoter; 2) a heterologous DNA sequence; and 3) a nucleotide sequence encoding TTV, a fragment of the nucleotide sequence or a complement of the nucleotide sequence or the fragment, wherein the heterologous DNA sequence is operably linked to the promoter. The promoter may be derived from TTV or from a heterologous source. The heterologous DNA sequence may encode a polynucleotide sequence that is complementary to a targeted RNA sequence. For example, the heterologous DNA sequence may encodes protein. The vector may be capable of being packaged into TTV particles for stable maintenance or expression of said heterologous DNA sequence.

The invention also includes a host cell comprising the above vector. The host cell may be eukaryotic.

Additionally, the invention includes a method of expressing the heterologous DNA sequence or a product encoded by the heterologous DNA sequence, in a host, comprising introducing the vector into a host for a time and under conditions sufficient for expression of the heterologous DNA sequence or product encoded thereby.

The invention also includes a method of detecting transmission of TTV from one individual to another comprising the steps of: (a) obtaining a biological sample from an individual having TTV; (b) isolating a TTV DNA sequence from the biological sample; (c) obtaining a biological sample from a second individual having TTV; (d) isolating a TTV DNA sequence from the biological sample of the second individual; (e) comparing the TTV DNA sequence of the first individual with the TTV DNA sequence of the second individual, identity between the DNA sequence of the first individual and the DNA sequence of the second individual indicating transmission of TTV from one individual to the other.

The invention also includes a method of determining TTV-infection in a tissue or organ prior to transplantation or xenotransplantation of the tissue or organ comprising the steps of:

(a) contacting a biological sample suspecting of containing a TTV target nucleotide sequence, from a potential donor animal, with a TTV primer pair represented by SEQ ID NO:60 and SEQ ID NO:61 to form a first reaction mixture; (b) contacting said reaction mixture with a TTV primer pair represented by SEQ ID NO:62 and SEQ ID NO:63 in order to form a second reaction mixture; and (c) detecting the presence of the TTV target nucleotide in the test sample, presence of the nucleotide indicating TTV-infection in the biological sample and in the tissue or organ.

The invention also includes a method of determining TTV-infection in a tissue or organ prior to transplantation or xenotransplantation of the tissue

or organ comprising the steps of: (a) contacting a biological sample suspecting of containing a TTV target nucleotide sequence, from a potential donor animal, with a TTV primer pair represented by SEQ ID NO:64 and SEQ ID NO:65, to form a first reaction mixture; (b) contacting the reaction mixture with a TTV primer pair represented by SEQ ID NO:66 and SEQ ID NO:67; and c) detecting the presence of the TTV target nucleotide in the test sample, presence of the nucleotide indicating TTV-infection in the biological sample and in the tissue or organ.

Additionally, a method of determining TTV-infection in a tissue or organ prior to transplantation or xenotransplantation of said tissue or organ comprising the steps of:

(a) contacting a biological sample suspecting of containing a TTV target nucleotide sequence, from a potential donor animal, with a TTV primer pair represented by SEQ ID NO:68 and SEQ ID NO:69, to form a first reaction mixture;

(b) contacting said reaction mixture with a TTV primer pair represented by SEQ ID NO:70 and SEQ ID NO:71; and

(c) detecting the presence of the TTV target nucleotide in said test sample, presence of said nucleotide indicating TTV-infection in said biological sample and in said tissue or organ. In the above-mentioned methods, the biological sample may be selected from the group consisting of blood, tissue and an organ.

Additionally, the invention includes a method of detecting the presence of target TTV nucleotides in a test sample, comprising the steps of:

(a) contacting a test sample suspecting of containing a target TTV nucleotide with a primer pair represented by SEQ ID NO:60 and SEQ ID NO:61, to form a reaction mixture; (b) contacting said reaction mixture with at least one TTV probe selected from the group consisting of SEQ ID NO:62 and SEQ ID NO:63; and (c) detecting the presence of said target TTV nucleotide in said test sample. In yet another embodiment of the method, the test sample may be contacted with a primer pair represented by SEQ ID NO:64 and SEQ ID NO:65 and the resulting reaction mixture contacted with at least one TTV probe selected from the group consisting of SEQ ID NO:66 and SEQ ID NO:67. In yet another embodiment, the test sample may be contacted with primer pair SEQ ID NO:68 and SEQ ID NO:69 and the resulting reaction mixture contacted with at least one TTV probe selected from the group consisting of SEQ ID NO:70 and SEQ ID NO:71. In the above-mentioned embodiments, at least one TTV probe may be conjugated to a detectable signal-generating compound. Such a compound is selected from the group consisting of a chemiluminescent compound, fluorescein and an enzyme. In the alternative, the TTV probe may be conjugated to an antibody.

The invention also includes a method of detecting TTV target nucleotides which may be present in a test sample comprising contacting the test sample suspected of containing a target TTV nucleotide sequence with a TTV primer pair consisting of 1) a primer selected

from the group consisting of: SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, and SEQ ID NO:70, and 2) a primer selected from the group consisting: SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, and SEQ ID NO:71, to form a reaction mixture which generates a product. In another embodiment, the method further comprises the steps of a) contacting the reaction mixture with a TTV primer pair consisting of: 1) a primer selected from the group consisting of: SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, and SEQ ID NO:70, wherein the nucleotide sequence of the selected primer hybridizes with the product of the reaction mixture and 2) a primer selected from the group consisting: SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, and SEQ ID NO:71, wherein the nucleotide sequence of the selected primer hybridizes with the product of the reaction mixture, and b) detecting the presence of the TTV target nucleotide in the test sample.

The present invention provides novel TT virus (TTV) DNA oligomer primers and probes. These DNA primers and probes are identified as SEQUENCE ID NOS. 60-71.

The present invention also provides an assay for detecting the presence of TTV in a test sample, which comprises (a) contacting a test sample suspected of containing a target TTV DNA sequence with a pair of TTV primers selected from the group consisting of the pair of SEQUENCE ID NOS. 60 and 61, followed by the pair of SEQUENCE ID NOS. 62 and 63; or the pair of

SEQUENCE ID NOS. 64 and 65, followed by the pair of SEQUENCE ID NOS. 66 and 67; or the pair of SEQUENCE ID NOS. 68 and 69, followed by the pair of SEQUENCE ID NOS. 70 and 71, and (b) detecting the presence of the target DNA in the test sample. The TTV primers can be conjugated to a signal generating compound. This signal generating compound is selected from the group consisting of a chemiluminescent compound, a fluorescein compound and an enzyme. The reaction can be performed on a solid phase. Each primer can be attached to a different hapten such as adamantane and carbazole.

Also provided is a test kit for detecting target TTV DNA in a test sample, comprising (a) a container containing a TTV primer, wherein the primer is selected from the group consisting of the pair of SEQUENCE ID NOS. 60 and 61, followed by the pair of SEQUENCE ID NOS. 62 and 63; or the pair of SEQUENCE ID NOS. 64 and 65, followed by the pair of SEQUENCE ID NOS. 66 and 67; or the pair of SEQUENCE ID NOS. 68 and 69, followed by the pair of SEQUENCE ID NOS. 70 and 71, and (b) a container containing a detection reagents. The TTV primers can be conjugated to a detectable signal generating compound. This signal generating compound is selected from the group consisting of a chemiluminescent compound, a fluorescein compound and an enzyme. The reaction can be performed on a solid phase. Each primer primer can be attached to a different hapten such as adamantane and carbazole.

Also provided is the proposed use of the TTV genome, or parts thereof, to construct a vector for expression of cloned genes in culture or in gene therapy treatment. The vector can consist of the

entire viral genome, either modified or wild type. It can also consist of parts of the genome such as the replication origin, specific genes, promoters or other control elements either by themselves or in conjunction with non-TTV sequences. A vector family is also proposed. The family would consist of identical sequences except for variable region(s) that prohibit re-infection of a previously infected host. The variable region(s) might encode epitopes from TTV isolates that do not show shared immunity, thus allowing multiple or prolonged treatment protocols.

Further provided is the use of TTV genomic diversity as a traceable marker to follow transmission of the virus between individuals, such traceability to be used in epidemiological or forensic studies.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGURE 1 shows the sensitivity of the TTV genome to mung bean nuclease where the log copy number of single stranded phagmid DNA (ssDNA) or double stranded plasmid DNA (dsDNA) present in control MBN digests are displayed.

FIGURE 2 shows TTV circular genome, where (A) displays the N22 clone sequence (gray box) described by Nishizawa et al., the anchored PCR extension clones extending upstream (u1) and downstream (d1) from N22, the inverse PCR product (ud) that overlaps the anchored PCR products, and the 113 nucleotide sequence identified in the GH1 (crosshatched box), and where (B) displays the initial 260 base region analyzed (Example 5), the amplicons obtained during genomic extension (thin lines), and the approximate position and orientation of conserved ORFs.

FIGURE 3 shows the distribution of the pairwise genetic distances observed between 157 TTV nucleotide sequences.

FIGURE 4 shows a consensus phylogenetic tree (unrooted) of 260 nucleotides from 163 TTV isolates where genetic groups are indicated as genotypes 1, 2, and 3 and subtypes 2.1 and 2.2; sequences isolated from a single individual are designated with the isolate number followed by the lower case letters a, b, or c; and geographical designations (AR, Argentina; EG, Egypt; GE, Greece; GH, Ghana; JA, Japan; NL, Netherlands; NZ, New Zealand; US, United States), and bootstrap values at the nodes for 1000 resamplings of the data are displayed.

FIGURE 5 shows the percent identity plotted across the alignments of seven full length TT virus nucleotide sequences within a sliding window of analysis of 50 positions where the dashed lines represent the mean identity across the entire length analyzed.

FIGURE 6 shows the unrooted phylogenetic tree generated from an alignment of seven full length and four near full length TT virus nucleotide sequences where bootstrap values are shown near the appropriate nodes for 1000 resamplings of the data and genotypes 1a, 1b, 2, and 3 are indicated.

FIGURE 7 shows a phylogenetic tree representing the genetic groupings of TT virus sequences generated with a conserved set of TT virus primersdescribed in example 7 where human isolates (Ghana, GH; Japan, JA; H, hemophiliac; United States, US), non-human isolates (Bovine, B; Chicken, C; Pan troglodytes, CH; Porcine,

P; Aotus trivirgatus, OW; Ovine, S; Saguinus labiatus, T), and boot strap values are displayed.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to novel DNA oligomer primers and probes, methods of utilizing these primers and/or probes, test kits which comprise these primers and/or probes, and diagnostic methods for determining the presence of TTV target nucleotide sequences in human and in animals. Also provided are the use of TTV nucleotide sequences as nucleic acid vectors, the use of TTV nucleotide sequences for testing prior to transplantation or xenotransplantation, and the use of TTV nucleotide sequences as markers for determining the route of TTV transmission between individuals.

More specifically, portions of the nucleic acid sequences derived from TTV are useful as primers or probes to determine the presence of TTV in test samples, and to isolate naturally occurring variants. These sequences also make available polypeptide sequences of TTV antigens encoded within the TTV genome(s) and permit the production of polypeptides which are useful as standards or reagents in diagnostic tests and/or as components of vaccines. Isolation and sequencing of other portions of the TTV genome also can be accomplished by utilizing PCR primers and/or probes derived from these nucleic acid sequences, thus allowing additional primers, probes and polypeptides of the TTV to be established, which will be useful in the diagnosis and/or treatment of TTV, both as a prophylactic and therapeutic agent. These nucleic acid primers and probes are identified

as SEQUENCE ID NOS. 52-59 and 60-71. These primers and probes hybridize to TTV sequence, or their complement, in regions of high sequence conservation. Thus, these primers and probes can be used in PCR assays to specifically and efficiently amplify TTV sequences with the reduced likelihood of failed amplification (and false-negative assay results) due to primer mismatches.

The present invention also provides test kits containing reagents which can be used for the detection of the presence and/or amount of polynucleotides derived from TTV. The test kit may comprise, for example, one or more containers such as vials or bottles, with each container containing a separate reagent such as a nucleic acid primer, probe or a cocktail of nucleic acid primers or probes. Other components such as buffers, controls, and the like, known to those of ordinary skill in art, may be included in such test kits.

The term "TT Virus" or "TTV", as used herein, collectively denotes a viral species, and attenuated strains or defective interfering particles derived therefrom. This virus may be transmitted via person to person contact (including sexual transmission, respiratory and parenteral routes) or via intraveneous drug use. The methods as described herein will allow the identification of individuals who have acquired TTV. As described herein, the TTV genome is comprised of DNA. Analysis of the nucleotide sequence and deduced amino acid sequence of the TTV reveals that viruses of this group have a genome organization similar to yet distinct from that of the Circoviridae family. Similar to the Circoviridae, TTV is a non-enveloped virus which contains a single-stranded

circular DNA genome. However, it should be noted that TTV demonstrated no sequence similarity with members of the Circoviridae based upon comparison of nucleic acid or deduced amino acid sequences using the BLAST algorithms, and the TTV virion and genome are much larger than those found for the Circoviridae. Thus, in view of the above, TTV, for purposes of the present invention, has been assigned to the family or genus Circinoviridae.

The term "similarity" and/or "identity" are used herein to describe the degree of relatedness between two polynucleotides or polypeptide sequences. The techniques for determining amino acid sequence "similarity" and/or "identity" are well-known in the art and include, for example, directly determining the amino acid sequence and comparing it to the seqeunces provided herein; determining the nucleotide sequence of the genomic material of TTV, and determining the amino acid sequence encoded therein, and comparing the corresponding regions. In general, by "identity" is meant the exact match-up of either the nucleotide sequence of TTV and that of another strain(s) or the amino acid sequence of TTV and that of another strain(s) at the appropriate place on each genome. Also, in general, by "similarity" is meant the exact match-up of amino acid sequence of TTV and that of another strain(s) at the appropriate place, where the amino acids are identical or possess similar chemical and/or physical properties such as charge or hydrophobicity. The programs available in the Wisconsin Sequence Analysis Package, Version 9 (available from the Genetics Computer Group, Madison, Wisconsin, 53711), for example, the GAP program, are capable of calculating both the identity and

similarity between two polynucleotide or two polypeptide sequences. Specifically, the GAP program uses the algorithm of Needleman and Wunsch (J. Mol. Biol. 48:443-453 (1970)) with the default penalties for gap creation and gap extension set at 50 and 3, respectively, for nucleotide alignments, and with the default penalties for gap creation and gap extension set at 12 and 4, respectively, for amino acid alignments. Other programs for calculating identity and similarity between two sequences such as FASTA (Pearson and Lipman, Proc. Natl. Acad. Sci. USA 85:24444-2448 (1988) and BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) are known in the art.

Additionally, several parameters are applicable, either alone or in combination, in identifying a strain of TTV. For example, it is expected that the overall nucleotide sequence identity of the genomes between TTV strains will be about 45% or greater, since it is now believed that the TTV strains may be genetically related, preferably about 60% or greater, and more preferably, about 80% or greater.

Also, it is expected that the overall sequence identity of the genomes between TTV strains at the amino acid level will be about 35% or greater since it is now believed that the TTV strains may be genetically related, preferably about 40% or greater, more preferably, about 60% or greater, and even more preferably, about 80% or greater. In addition, there will be corresponding contiguous sequences of at least about 13 nucleotides, which may be provided in combination of more than one contiguous sequence.

A polynucleotide "derived from" a designated sequence for example, the TTV DNA, or from the TTV genome, refers to a polynucleotide sequence which is

comprised of a sequence of approximately at least about 6 nucleotides, is preferably at least about 8 nucleotides, is more preferably at least about 10-12 nucleotides, and even more preferably is at least about 15-20 nucleotides corresponding, and is similar to, or complementary to, a region of the designated nucleotide sequence. Preferably, the sequence of the region from which the polynucleotide is derived is similar to, or complementary to, a sequence which is unique to the TTV genome. Whether or not a sequence is similar to, or complementary to, a sequence which is unique to a TTV genome, can be determined by techniques known to those skilled in the art. Comparisons to sequences in databanks, for example, can be used as a method to determine the uniqueness of a designated sequence. Regions from which sequences may be derived include but are not limited to regions encoding specific epitopes, as well as non-translated and/or non-transcribed regions.

The derived polynucleotide will not necessarily be derived physically from the nucleotide sequence of TTV, but may be generated in any manner, including but not limited to chemical synthesis, replication or reverse transcription or transcription, which are based on the information provided by the sequence of bases in the region(s) from which the polynucleotide is derived. In addition, combinations of regions corresponding to that of the designated sequence may be modified in ways known in the art to be consistent with an intended use.

The terms "polynucleotide," "oligomer" and "oligonucleotide" are used interchangeably herein. The term "polynucleotide" as used herein means a polymeric form of nucleotides of any length, either

ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, the term includes double- and single-stranded DNA, as well as double- and single-stranded RNA. It also includes modifications, either by methylation and/or by capping, and unmodified forms of the polynucleotide.

"TTV containing a sequence corresponding to a DNA" means that the TTV contains a polynucleotide sequence which is similar to or complementary to a sequence in the designated DNA. The degree of similarity or complementarity to the DNA will be approximately 50% or greater, will preferably be at least about 70%, and even more preferably will be at least about 90%. The sequence which corresponds will be at least about 70 nucleotides, preferably at least about 80 nucleotides, and even more preferably at least about 90 nucleotides in length. The correspondence between the TTV and the DNA can be determined by methods known in the art, and include, for example, a direct comparison of the sequenced material with the DNAs described, or hybridization and digestion with single strand nucleases, followed by size determination of the digested fragments.

"Purified viral polynucleotide" refers to a TTV genome or fragment thereof which is essentially free, i.e., contains less than about 50%, preferably less than about 70%, and even more preferably, less than about 90% of polypeptides with which the viral polynucleotide is naturally associated. Techniques for purifying viral polynucleotides are well known in the art and include, for example, disruption of the particle with a chaotropic agent, and separation of the polynucleotide(s) and polypeptides by ion-exchange

chromatography, affinity chromatography, and sedimentation according to density. Thus, "purified viral polypeptide" means a TTV polypeptide or fragment thereof which is essentially free, that is, contains less than about 50%, preferably less than about 70%, and even more preferably, less than about 90% of of cellular components with which the viral polypeptide is naturally associated. Methods for purifying are known to the routineer.

"Polypeptide" as used herein indicates a molecular chain of amino acids and does not refer to a specific length of the product. Thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide. This term, however, is not intended to refer to post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like.

The term "open reading frame" or "ORF" refers to a region of a polynucleotide sequence which encodes a polypeptide; this region may represent a portion of a coding sequence or a total coding sequence.

A "coding sequence" is a polynucleotide sequence which is transcribed into mRNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the 5' -terminus and a translation stop codon at the 3' -terminus. A coding sequence can include, but is not limited to, mRNA, cDNA, and recombinant polynucleotide sequences.

The term "immunologically identifiable with/as" refers to the presence of epitope(s) and polypeptide(s) which also are present in, and are unique to, the designated polypeptide(s), usually TTV

proteins. Immunological identity may be determined by antibody binding and/or competition in binding. These techniques are known to the routineer and also are described herein. The uniqueness of an epitope also can be determined by computer searches of known data banks, such as GenBank®, for the polynucleotide sequences which encode the epitope, and by amino acid sequence comparisons with other known proteins.

As used herein, "epitope" means an antigenic determinant of a polypeptide. Conceivably, an epitope can comprise three amino acids in a spatial conformation which is unique to the epitope. Generally, an epitope consists of at least five such amino acids, and more usually, it consists of at least eight to ten amino acids. Methods of examining spatial conformation are known in the art and include, for example, x-ray crystallography and two-dimensional nuclear magnetic resonance.

The term "individual" as used herein refers to vertebrates, particularly members of the mammalian species and includes but is not limited to domestic animals, sports animals, primates and humans; more particularly the term refers to tamarins, chimpanzees and humans.

The term "plus strand" (or "+") as used herein denotes a nucleic acid that contains the sequence that encodes the polypeptide. The term "minus strand" (or "-") denotes a nucleic acid that contains a sequence that is complementary to that of the "plus" strand.

A "positive stranded genome" virus denotes that the genome, whether RNA or DNA, is single-stranded and encodes a viral polypeptide(s).

A "negative stranded genome" virus denotes that the genome, whether RNA or DNA, is single-stranded and is complementary to that of the "plus" strand.

The term "test sample" refers to a component of an individual's body which is the source of the analyte (such as, antibodies of interest, antigens of interest or polynucleotides of interest). These components are well known in the art. These test samples include biological samples which can be tested by the methods of the present invention described herein and include human and animal body fluids such as whole blood, serum, plasma, cerebrospinal fluid, urine, lymph fluids, and various external secretions of the respiratory, intestinal and genitorurinary tracts, tears, saliva, milk, white blood cells, myelomas and the like; biological fluids such as cell culture supernatants; fixed tissue specimens; and fixed cell specimens.

"Purified TTV" refers to a preparation of TTV which has been isolated from the cellular constituents with which the virus is normally associated, and from other types of viruses which may be present in the infected tissue. The techniques for isolating viruses are known to those skilled in the art and include, for example, centrifugation and affinity chromatography.

"Solid phases" ("solid supports") are known to those in the art and include the walls of wells of a reaction tray, test tubes, polystyrene beads, magnetic beads, nitrocellulose strips, membranes, microparticles such as latex particles, sheep (or other animal) red blood cells, duracytes and others. The "solid phase" is not critical and can be selected by one skilled in the art. Thus, latex particles, microparticles, magnetic or non-magnetic beads,

membranes, plastic tubes, walls of microtiter wells, glass or silicon chips, sheep (or other suitable animal's) red blood cells and duracytes are all suitable examples. Suitable methods for immobilizing capture reagents on solid phases include ionic, hydrophobic, covalent interactions and the like. A "solid phase", as used herein, refers to any material which is insoluble, or can be made insoluble by a subsequent reaction. The solid phase can be chosen for its intrinsic ability to attract and immobilize the capture reagent. Alternatively, the solid phase can retain an additional receptor which has the ability to attract and immobilize the capture reagent. The additional receptor can include a charged substance that is oppositely charged with respect to the capture reagent itself or to a charged substance conjugated to the capture reagent. As yet another alternative, the receptor molecule can be any specific binding member which is immobilized upon (attached to) the solid phase and which has the ability to immobilize the capture reagent through a specific binding reaction. The receptor molecule enables the indirect binding of the capture reagent to a solid phase material before the performance of the assay or during the performance of the assay. The solid phase thus can be a plastic, derivatized plastic, magnetic or non-magnetic metal, glass or silicon surface of a test tube, microtiter well, sheet, bead, microparticle, chip, sheep (or other suitable animal's) red blood cells, duracytes and other configurations known to those of ordinary skill in the art.

It is contemplated and within the scope of the invention that the solid phase also can comprise any

suitable porous material with sufficient porosity to allow access by detection antibodies or polynucleotides, and a suitable surface affinity to bind antigens or polynucleotides. Microporous structures are generally preferred, but materials with gel structure in the hydrated state may be used as well. Such useful solid supports include but are not limited to natural polymeric carbohydrates and their synthetically modified, cross-linked or substituted derivatives, such as agar, agarose, cross-linked alginic acid, substituted and cross-linked guar gums, cellulose esters, especially with nitric acid and carboxylic acids, mixed cellulose esters, and cellulose ethers; natural polymers containing nitrogen; synthetic polymers which may be prepared with suitably porous structures, such as vinyl polymers; porous inorganic materials such as sulfates or carbonates of alkaline earth metals and magnesium, including barium sulfate, calcium sulfate, calcium carbonate, silicates of alkali and alkaline earth metals, aluminum and magnesium; and aluminum or silicon oxides or hydrates, such as clays, alumina, talc, kaolin, zeolite, silica gel, or glass (these materials may be used as filters with the above polymeric materials); and mixtures or copolymers of the above classes, such as graft copolymers obtained by initializing polymerization of synthetic polymers on a pre-existing natural polymer. All of these materials may be used in suitable shapes such as films, sheets, beads or plates, or they may be coated onto or bonded or laminated to appropriate inert carriers, such as paper, glass, plastic films, or fabrics.

The porous structure of nitrocellulose has excellent absorption and adsorption qualities for a wide variety of reagents. Nylon also possesses similar characteristics and also is suitable. It is contemplated that such porous solid supports described hereinabove are preferably in the form of sheets of thickness from about 0.01 to 0.5 mm, preferably about 0.1 mm. The pore size may vary within wide limits, and is preferably from about 0.025 to 15 microns, especially from about 0.15 to 15 microns. The surfaces of such supports may be activated by chemical processes which cause covalent linkage of the antigen, antibody or polynucleotide to the support. The irreversible binding of the antigen or antibody is obtained, however, in general, by adsorption on the porous material by poorly understood hydrophobic forces. Suitable solid supports also are described in U.S. Patent No. 5,075,077.

The "indicator reagent "comprises a "signal generating compound" (also termed a "label") generates a measurable signal detectable by external means conjugated (attached) to a specific binding member for TTV. "Specific binding member" as used herein means a member of a specific binding pair. That is, two different molecules where one of the molecules through chemical or physical means specifically binds to the second molecule. In addition to being an antibody member of a specific binding pair for TTV, the indicator reagent also can be a member of any specific binding pair, including either hapten-anti-hapten systems such as biotin or anti-biotin, avidin or biotin, a carbohydrate or a lectin, a complementary nucleotide sequence, an effector or a receptor molecule, an enzyme cofactor and an enzyme, an enzyme

inhibitor or an enzyme, and the like. Furthermore, specific binding pairs can include members that are analogs of the original specific binding members, for example, an analyte-analog. An immunoreactive specific binding member can be an antibody or fragment thereof, an antigen or fragment thereof, or an antibody/antigen complex including those formed by recombinant DNA molecules that bind either to TTV as in a sandwich assay, to the capture reagent as in a competitive assay, or to the ancillary specific binding member as in an indirect assay.

The various "signal generating compounds" (labels) contemplated include chromogens, catalysts such as enzymes, luminescent compounds such as fluorescein and rhodamine, chemiluminescent compounds such as dioxetanes, acridiniums, phenanthridiniums and luminol, radioactive elements, and direct visual labels. Examples of enzymes include alkaline phosphatase, horseradish peroxidase, beta-galactosidase, and the like. The selection of a particular label is not critical, but it will be capable of producing a signal either by itself or in conjunction with one or more additional substances.

The term "detection label" refers to a molecule or moiety having a property or characteristic which is capable of detection. A detection label can be directly detectable as with, for example, radioisotopes, fluorophores, chemiluminophores, enzymes, colloidal particles, fluorescent microparticles and the like; or a label may be indirectly detectable as with, for example, specific binding members. It will be understood that direct labels may require additional components such as, for example, substrates, triggering reagents, light, and

the like to enable detection of the label. When indirect labels are used for detection, they are typically used in combination with a conjugate. A "conjugate" is typically a specific binding member which has been attached or coupled to a directly detectable label. Similar to the synthesis of solid phase reagents, coupling chemistries for synthesizing a conjugate are well known in the art and can include, for example, any chemical means and/or physical means that does not destroy the specific binding property of the specific binding member or the detectable property of the label.

The term "hapten", as used herein, refers to a partial antigen or non-protein binding member which binds to an antibody, but which does not elicit antibody formation unless coupled to a carrier protein. Examples of haptens include biotin, avidin, adamantane and carbazole.

"Analyte," as used herein, is the substance to be detected which may be present in the test sample. The analyte can be any substance for which there exists a naturally occurring specific binding member (such as an antibody), or for which a specific binding member can be prepared (such as a polynucleotide). Thus, an analyte is a substance that can bind to one or more specific binding members in an assay. "Analyte" also includes target nucleotide sequences and any antigenic substances such as haptens, antibodies and combinations thereof. As a member of a specific binding pair, the analyte can be detected by means of naturally occurring specific binding partners (pairs) such as the use of intrinsic factor protein as a member of a specific binding pair for the determination of Vitamin B12, the use of folate-

binding protein to determine folic acid, or the use of a lectin as a member of a specific binding pair for the determination of a carbohydrate. The analyte can include a protein, a peptide, an amino acid, a nucleotide target, and the like.

Embodiments which utilize ion capture procedures for immobilizing an immobilizable reaction complex with a negatively charged polymer, described in EP publication 0326100 and EP publication no. 0406473, can be employed according to the present invention to effect a fast solution-phase immunochemical reaction. An immobilizable immune complex is separated from the rest of the reaction mixture by ionic interactions between the negatively charged poly-anion/immune complex and the previously treated, positively charged porous matrix and detected by using various signal generating systems previously described, including those described in chemiluminescent signal measurements as described in EPO Publication No. 0273115.

Also, the methods of the present invention can be adapted for use in systems which utilize microparticle technology including in automated and semi-automated systems wherein the solid phase comprises a microparticle (magnetic or non-magnetic). Such systems include those described in U.S. Patent No. 5,244,630 and U.S. Patent No. 5,089,424 which correspond to published EPO application Nos. EP 0425633 and EP 0424634, respectively.

The use of scanning probe microscopy (SPM) for analyte detection also is adaptable. In scanning probe microscopy, in particular in atomic force microscopy, the capture phase is adhered to a solid phase and a scanning probe microscope is utilized to

detect antigen/antibody complexes which may be present on the surface of the solid phase. The use of scanning tunnel microscopy eliminates the need for labels that normally must be utilized in many immunoassay systems to detect antigen/antibody complexes. Such a system is described in U.S. patent application Serial No. 07/662,147, now abandoned.

It is contemplated and within the scope of the present invention that the TTV group of viruses may be detectable in assays by use of synthetic, recombinant or native primers or probes that are common to all TT viruses (termed "universal" primers or probes). It also is within the scope of the present invention that different synthetic, recombinant or native primers or probes identifying different regions from the TTV genome can be used in assay formats. Such assay formats are known to those of ordinary skill in the art and are discussed hereinbelow.

Using determined portions of the isolated TTV nucleic acid sequences as a basis, oligomers of approximately eight nucleotides or more can be prepared, either by excision or synthetically, which hybridize with the TTV genome. Such oligomers are useful in identification of the viral agent(s), further characterization of the viral genome, as well as in detection of the virus(es) in diseased individuals. The natural or derived primers or probes for TTV polynucleotides are a length that allows the detection of unique viral sequences. While six to eight nucleotides may be a workable length, sequences of ten to twelve nucleotides are preferred, and those of about 20 nucleotides may be most preferred. These sequences preferably will derive from regions that

lack heterogeneity. These primers or probes can be prepared using routine, standard methods including automated oligonucleotide synthetic methods. A complement of any unique portion of the TTV genome will be satisfactory. Complete complementarity is desirable for use as primers or probes, although it may be unnecessary as the length of the primers or probes is increased.

When used as diagnostic reagents, the test sample to be analyzed, such as blood or serum, may be treated such as to extract the nucleic acids contained therein. The resulting nucleic acid from the sample may be subjected to amplification techniques such as Ligase Chain Reaction (LCR), Polymerase Chain Reaction (PCR), Q-beta replicase, NASBA, etc.

The primers or probes can be made completely complementary to the TTV genome. Therefore, usually high stringency conditions are desirable in order to prevent false positives. However, conditions of high stringency should be used only if the primers or probes are complementary to regions of the TTV genome that lack heterogeneity. The stringency of annealing is determined by a number of other factors, including temperature, ionic strength, primer or probe length and primer probe concentration.

It is contemplated that the TTV genome sequences may be present in serum of infected individuals at relatively low levels, for example, approximately 10^2-10^3 sequences per milliliter. This level may require that amplification techniques, such as the LCR or the PCR, be used in detection assays. The amplified sequence(s) then may be detected using an assay such as those known in the art. The primers or probes can be packaged in diagnostic kits which include the

primer or probe nucleic acid sequences, which sequences may be labeled; alternatively, the primers or probes may be unlabelled and the ingredients for labeling could be included with the kit. The kit also may contain other suitably packaged reagents and materials needed or desirable for the particular amplification protocol, for example, standards as well as instructions for performing the assay.

Other known amplification methods which can be utilized herein include but are not limited to the so-called "NASBA" or "3SR" technique taught in PNAS USA 87:1874-1878 (1990) and also discussed in Nature:350 (No. 6313):91-92 (1991) and Q-beta replicase.

PCR amplification also can be performed *in situ* utilizing the reagents described herein. *In situ* PCR involves taking morphologically intact tissues, cells or chromosomes through the nucleic acid amplification process to demonstrate the presence of a particular piece of genetic information. Since it does not require homogenization of cells and extraction of the target sequence, it provides precise localization and distribution of a sequence in cell populations. *In situ* amplification can identify the sequence of interest concentrated in the cells containing it. It also can identify the type and fraction of the cells in a heterogeneous cell population containing the sequence of interest. Both DNA and RNA can be detected.

Assays as described herein may utilize one viral antigen derived from any clone-containing TTV nucleic acid sequence, or from the composite nucleic acid sequences derived from the TTV nucleic acid sequences in these clones, or from the TTV genome from which the nucleic acid sequences in these clones are derived.

Or, the immunoassay may use a combination of viral antigens derived from these sources. It also may use, for example, a monoclonal antibody directed against the same viral antigen, or polyclonal antibodies directed against different viral antigens. Assays can include but are not limited to those based on competition, direct reaction or sandwich-type assays. Assays may use solid phases or may be performed by immunoprecipitation or any other methods which do not utilize solid phases. Examples of assays which utilize labels as the signal generating compound and those labels are described herein. Signals also may be amplified by using biotin and avidin, enzyme labels or biotin anti-biotin systems, such as that described in pending U.S. patent application Serial Nos. 08/608,849, now abandoned; 08/070,647, now abandoned; 08/418,981, now abandoned; and 08/687,785, now abandoned.

It should be noted that any of the diagnostic assays described herein may be utilized in connection with humans or animals. For example, one may wish to determine whether an animal (e.g., a goat, a dog, a cat, a cow, or a horse) has been exposed to the virus and act accordingly with respect to administration of anti-viral agents. Additionally, one may wish to administer vectors to the animal and thereby carry out gene therapy. Since animals have many of the same therapeutic needs and physical conditions as humans, the applicability of the methods described herein to animals as well as humans is quite apparent and is encompassed within the scope of the invention.

It should be noted that the TTV nucleic acid sequences may also be used to gain further information on the sequence of the TTV genome, and for

identification and isolation of the TTV agent. Thus, it is contemplated that this knowledge will aid in the characterization of TTV including the nature of the TTV genome, the structure of the viral particle, and the nature of the antigens of which it is composed. This information, in turn, can lead to additional polynucleotide primers, polypeptides derived from the TTV genome, and antibodies directed against TTV epitopes useful for the diagnosis and/or treatment of TTV infections.

Synthetic oligonucleotides may be prepared using an automated oligonucleotide synthesizer such as that described by Warner, DNA 3:401 (1984). If desired, the synthetic strands may be labeled with ^{32}P by treatment with polynucleotide kinase in the presence of ^{32}P-ATP, using standard conditions for the reaction. DNA sequences including those isolated from genomic or libraries, may be modified by known methods which include site directed mutagenesis as described by Zoller, Nucleic Acids Res. 10:6487 (1982). Briefly, the DNA to be modified is packaged into phage as a single stranded sequence, and converted to a double stranded DNA with DNA polymerase using, as a primer, a synthetic oligonucleotide complementary to the portion of the DNA to be modified, and having the desired modification included in its own sequence. Culture of the transformed bacteria, which contain replications of each strand of the phage, are plated in agar to obtain plaques. Theoretically, 50% of the new plaques contain phage having the mutated sequence, and the remaining 50% have the original sequence. Replicates of the plaques are hybridized to labeled synthetic probe at temperatures and conditions suitable for hybridization with the correct strand, but not with

the unmodified sequence. The sequences which have been identified by hybridization are recovered and cloned.

Polymerase chain reaction (PCR) and ligase chain reaction (LCR) are techniques for amplifying any desired nucleic acid sequence (target) contained in a nucleic acid or mixture thereof. In PCR, a pair of primers are employed in excess to hybridize at the outside ends of complementary strands of the target nucleic acid. The primers are each extended by a polymerase using the target nucleic acid as a template. The extension products become target sequences themselves, following dissociation from the original target strand. New primers are then hybridized and extended by a polymerase, and the cycle is repeated to geometrically increase the number of target sequence molecules. PCR is disclosed in U.S. Patent No. 4,683,195 and No. 4,683,202.

LCR is an alternate mechanism for target amplification. In LCR, two sense (first and second) probes and two antisense (third and fourth) probes are employed in excess over the target. The first probe hybridizes to a first segment of the target strand and the second probe hybridizes to a second segment of the target strand, the first and second segments being positioned so that the primary probes can be ligated into a fused product. Further, a third (secondary) probe can hybridize to a portion of the first probe and a fourth (secondary) probe can hybridize to a portion of the second probe in a similar ligatable fashion. If the target is initially double stranded, the secondary probes will also hybridize to the target complement in the first instance. Once the fused strand of sense and antisense probes are separated

from the target strand, it will hybridize with the third and fourth probes which can be ligated to form a complementary, secondary fused product. The fused products are functionally equivalent to either the target or its complement. By repeated cycles of hybridization and ligation, amplification of the target sequence is achieved. This technique is described in EP-A-320,308, hereby incorporated by reference. Other aspects of LCR technique are disclosed in EP-A-439,182, which is incorporated herein by reference.

In one embodiment, the present invention generally comprises the steps of contacting a test sample suspected of containing a target TTV nucleotide sequence with amplification reaction reagents comprising an amplification primer pair, that can hybridize with a region of the TTV sequences, followed by amplification with another set of primers. (Alternatively, a primer pair may be used followed by the use of a probe.) Primers and probes employed according to the methods herein may be labeled with capture and detection labels wherein one primer of the initial pair is labeled with one type of label and one primer of the second pair (or sole probe) is labeled with the other type of label.

After the amplicon products are formed, they are detected by gel electrophoresis and visualization with ethidium bromide as is know in the art. Alternatively, standard heterogeneous assay formats are suitable for detecting the products using the detection labels and capture labels present on the primers. The products can be bound to a solid phase reagent by virtue of the capture label and detected by virtue of the detection label. In cases where the

detection label is directly detectable, the presence of the products on the solid phase can be detected by causing the label to produce a detectable signal, if necessary, and detecting the signal. In cases where the label is not indirectly detectable, the captured products can be contacted with a conjugate, which generally comprises a binding member attached to a directly detectable label. The conjugate becomes bound to the complexes and the conjugate's presence on the complexes can be detected with the directly detectable label. Thus, the presence of the products on the solid phase reagent can be determined. Those skilled in the art will recognize that wash steps may be employed to wash away non-captured amplicon or primer as well as unbound conjugate.

A test sample is typically anything suspected of containing a target sequence. Test samples can be prepared using methodologies well known in the art such as by obtaining a specimen from an individual and, if necessary, disrupting any cells contained therein to release target nucleic acids. Although the target sequence is described as single stranded, it also is contemplated to include the case where the target sequence is actually double stranded but is merely separated from its complement prior to hybridization with the amplification primer sequences. In the case where PCR is employed in the preferred method, the ends of the target sequences are usually known. In cases where LCR or a modification thereof is employed in the preferred method, the entire target sequence is usually known. Typically, the target sequence is a nucleic acid sequence such as for example RNA or DNA.

The method provided herein can be used in well known amplification reactions that thermal cycle reaction mixtures, particularly in PCR and GLCR. Amplification reactions typically employ primers to repeatedly generate copies of a target nucleic acid sequence, which target sequence is usually a small region of a much larger nucleic acid sequence. Primers are themselves nucleic acid sequences that are complementary to regions of a target sequence. Under amplification conditions, these primers hybridize or bind to the complementary regions of the target sequence. Copies of the target sequence typically are generated by the process of primer extension and/or ligation which utilizes enzymes with polymerase or ligase activity, separately or in combination, to add nucleotides to the hybridized primers and/or ligate adjacent probe pairs. The nucleotides that are added to the primers or probes, as monomers or preformed oligomers, are also complementary to the target sequence. Once the primers or probes have been sufficiently extended and/or ligated they are separated from the target sequence, for example, by heating the reaction mixture to a "melt temperature" which is one where complementary nucleic acid strands dissociate. Thus, a sequence complementary to the target sequence is formed.

A new amplification cycle then can take place to further amplify the number of target sequences by separating any double stranded sequences, allowing primers or probes to hybridize to their respective targets, extending and/or ligating the hybridized primers or probes and re-separating. The complementary sequences that are generated by amplification cycles can serve as templates for primer

extension or filing the gap of two probes to further amplify the number of target sequences. Typically, a reaction mixture is cycled between 20 and 100 times, more typically, a reaction mixture is cycled between 25 and 50 times. The numbers of cycles can be determined by the routineer. In this manner, multiple copies of the target sequence and its complementary sequence are produced. Thus, primers initiate amplification of the target sequence when it is present under amplification conditions.

Generally, two primers which are complementary to a portion of a target strand and its complement are employed in PCR. For LCR, four probes, two of which are complementary to a target sequence and two of which are similarly complementary to the targets complement, are generally employed. In addition to the primer sets and enzymes previously mentioned, a nucleic acid amplification reaction mixture may also comprise other reagents which are well known and include but are not limited to: enzyme cofactors such as manganese; magnesium; salts; nicotinamide adenine dinucleotide (NAD); and deoxynucleotide triphosphates (dNTPs) such as for example deoxyadenine triphosphate, deoxyguanine triphosphate, deoxycytosine triphosphate and deoxythymine triphosphate.

Typically, the PCR primer sequences or the LCR probe sequences are in the range of between 20 and 50 nucleotides long, more typically in the range of between 20 and 30 nucleotides long.

Various methods for synthesizing primers and probes are well known in the art. Similarly, methods for attaching labels to primers or probes are also well known in the art. For example, it is a matter of routine to synthesize desired nucleic acid primers or

probes using conventional nucleotide phosphoramidite chemistry and instruments available from Applied Biosystems, Inc., (Foster City, CA), Dupont (Wilmington, DE), or Milligen (Bedford MA). Many methods have been described for labelling oligonucleotides such as the primers or probes of the present invention. Enzo Biochemical (New York, NY) and Clontech (Palo Alto, CA) both have described and commercialized oligo-labeling techniques. For example, a primary amine can be attached to a 3′ oligo terminus using 3'-Amine-ON CPG™ (Clontech, Palo Alto, CA). Similarly, a primary amine can be attached to a 5′ oligo terminus using Aminomodifier II® (Clontech). The amines can be reacted to various haptens using conventional activation and linking chemistries. In addition, U.S. patent application serial no. 08/625,566, now abandoned, and U.S. Patent No. 5,290,925, which are each incorporated herein by reference, teach methods for labeling oligos at their 5′ and 3′ termini, respectively. Publications WO92/10505, published 25 June 1992 and WO 92/11388 published 9 July 1992 teach methods for labeling oligos at their 5′ and 3′ ends respectively. According to one known method for labeling an oligonucleotide, a label-phosphoramidite reagent is prepared and used to add the label to the oligonucleotide during its synthesis. See, for example, N.T. Thuong et al., Tet. Letters 29(46):5905-5908 (1988); or J. S. Cohen et al., published U.S. Patent Application 07/246,688 (NTIS ORDER No. PAT-APPL-7-246,688) (1989). Preferably, oligos are labeled at their 3' and 5' ends.

Capture labels are carried by one or more of the primers (or the probe) and can be a specific binding

member which forms a binding pair with the solid phase reagent's specific binding member. It will be understood, of course that one or more primers and/or the probe itself may serve as the capture label. For example, in the case where a solid phase reagent's binding member is a nucleic acid sequence, it may be selected such that it binds a complementary portion of the primer or probe to thereby immobilize the primer or probe to the solid phase. In the case where the primer or probe itself serves as the capture label, at least a portion of the primer or probe will be free to hybridize with a nucleic acid on a solid phase.

Generally, amplicon members can be detected using techniques commonly employed to perform heterogeneous immunoassays. Preferably, in this embodiment, detection is performed according to the protocols used by the commercially available Abbott LCx® instrumentation (Abbott Laboratories; Abbott Park, IL).

The primers disclosed herein are useful in typical PCR assays, wherein the test sample is contacted with a pair of primers, amplification is performed, amplification then occurs with another pair of primers (or a probe is utilized) and the products are detected.

Another method proposed herein pertains to the use of the TTV genome, or parts thereof, in a nucleic acid vector suitable for expression of cloned genes, either in cell culture or in the context of gene therapy. A wide range of chimeric TTV-based vectors incorporating nucleic acid sequences from multiple sources could be constructed by one skilled in the art [Maniatis (1989) "Molecular Cloning: A Laboratory Manual"]. In particular, portions of the TTV genome

responsible for specific viral functions (e.g., replication, expression, virion formation), in conjunction with nucleic acid sequences that confer other desired traits, may be propagated as plasmid clones. The TTV sequence of interest may then be excised from the plasmid clone using appropriate restriction enzymes, and gel purified. A ligation reaction may then be performed containing the gel purified TTV sequence in conjunction with similarly prepared non-TTV nucleic acid sequences that confer other desired traits (e.g., the ability to replicate, and be selected for, in procaryotic cells). The desired ligation product may then be clone purified and confirmed by DNA sequencing. The amount of TTV present in such a vector may range from as few as 20 nucleotides up to the complete TTV genome. Furthermore, the TTV sequences used can be either wild type or modified, using commercially available *in vitro* mutagenesis kits, to alter specific properties such as vector capacity, efficiency of replication, host cell range, transmission and the like.

Alternatively, the entire TTV genome could be used, either in its wild type form or modified to alter specific properties such as vector capacity, efficiency of replication, host cell range, transmission and the like.

With respect to conditions for growth of TTV in cell culture, various cell lines (e.g., fibroblasts, hepatocytes, HeLa cells) and growth media may be tested for the ability to propagate the virus. Furthermore, studies may be done to establish the site(s) of TTV replication in animals and humans by testing for the presence, in various tissues, of the TTV "plus" strand (i.e. non-genomic strand). This

information is significant if the vector depends on TTV sequences for replication and/or transmission. Such information is not as important if the vector does not replicate within the host cell or transmission between cells, or if such functions are provided by other non-TTV sequences.

Introduction of the vector into cell culture may be achieved by several common methods known to those skilled in the art, including transformation or micro-injection of purified DNA into the cells, and infection of cells by virions containing the vector genome. Similarly, administration of the vectors to animals or humans could be accomplished by several methods. Purified vector DNA or infectious virions can be injected directly into the organism (e.g. intra-muscular or intravenous injection). Alternatively, cells into which the vector has been previously introduced (described above) can be injected into the organism, or infectious virions can be introduced through mucous membranes (e.g., in aerosol form through the lining of the lung).

Potential applications of a TTV-based vector are the same as for vectors already in use. This includes cell culture production of useful proteins, such as antigens for vaccines or diagnostic tests, and enzymes of clinical or research value. Gene therapy [Anderson (1992) "Human Gene Therapy", Science 256:808-813] for replacement of defective genes such as the LDL receptor for hypercholesterolemia [Wilson et al. (1990) "Prospects for Gene Therapy of Familial Hypercholesterolemia", Mol. Biol. Med. 7:223-232; Grossman et al. (1992) "Frontiers in Gene Therapy: LDL Receptor Replacement for Hypercholesterolemia", J. Lab. Clin. Med. 5:457-460] or hypoxanthine-guanine

phosphoribosyltransferase for gout [Davidson et al. (1989) "Human Hypoxanthine-guanine Phosphoribosyltransferase Deficiency: The Molecular Defect in a Patient with Gout ($HPRT_{ASHVILLE}$)", J. Biol. Chem. 264:520-525], are but a few of the conditions [Schwandt et al. (1989) "Genetic-disorders of Metabolism in Adults", Internist 30:547-555] possibly treatable with a TTV-based vector.

As used herein, the term "vector" refers to a nucleic acid sequence that can be ligated to other nucleic acid sequences, conferring on these other sequences any or all of the following: the ability to be introduced into cells, to be replicated within cells, and to be expressed within cells or to be transmitted between cells.

A family of closely related TTV vectors is also proposed. Members of the family would vary chiefly in those regions of the TTV genome that encode epitopes recognized by the immune system of a host, resulting in clearance of the vector. The epitope-encoding region for each vector would be derived from a TTV isolate that does not show shared immunity with any of the other members of the vector family. Existence of such non-cross reactive TTV isolates is strongly suggested by the demonstration of co-infections and the high prevalence level in humans. The appearance, then loss, of detectable TTV in an experimentally infected chimpanzee, and the common inability of DNA virus-based gene therapy to successfully repeat a second round in humans, suggests that immunity is a potential concern. Thus, the vector panel described above could be used to maintain or repeat treatment of an individual who has developed immunity to the initial vector.

A further method is proposed that relies on the high sequence diversity of the TTV genome. In this method TTV genomic DNA would be isolated from two or more individuals, amplified and sequenced, either partially or in full. Comparison of the sequences would then be performed across a region of known high variability. Furthermore, the region should be sufficiently large such that the chance of two isolates having the exact, or nearly exact, nucleic acid sequence is minimized. The more similar the TTV sequences are to one another, the more likely it is that the individuals involved were infected from a common source or that one individual infected the other. Therefor, even in a population with a high level of pre-existing TTV infections, studies can be done on the specific mode of transmission of TTV within social groups, or under controlled conditions.

Not only is this information useful from an epidemiological standpoint, but it also has applications to fields such as forensics. In this embodiment, TTV genomic sequence could be used to establish previous contact between individuals and, depending on the mode of transmission, what the nature of the contact was. In particular, existing data suggest that TTV can be transmitted by parenteral exposure. (Okamoto et al., Hepatology Research 10:1-16 (1998; Simmonds et al., The Lancet 352:191-194 (1998; Desai et al., J. Infect. Dis. in press:(1999)) Furthermore, the presence of TTV detected in fecal samples (Okamoto et al., J. of Med. Virol. 56:128-132 (1998)) suggests that this virus might also be spread by the fecal-oral oral route. In addition, it is conceivable that other routes of transmission are possible (e.g., sexual or aerosal). Additional

studies will be needed to address these possibilities. Of course, independent of how TTV is spread, the high level of sequence divergence noted among the isolates identified to date (see Example 5) implies that one could use the variability of the TTV genome to establish contact between people. For example, since TTV is transmitted parenterally, one could potentially determine whether intravenous drug users share contaminated needles. Similarly, if TTV is transmitted sexually, one could potentially demonstrate sexual contact between two individuals, months after such contact, by comparing TTV sequences. Thus, the TTV virus may be utilized for forensic purposes.

Moreover, xenotransplantation presents another area where assays for TTV may prove useful. Although xenogenic tissue grafts may help solve the current shortage of organ donation, the possible zoonosis of viruses from the transplanted organ is a concern (Curr. Opin. Immunol. 10:539-542 (1998)). Specifically, the presence of an animal virus in transplanted tissue may result in graft rejection or, due to the immunosupressed state of a transplant recipient, exacerbated disease and death. Therefore, identifying TTV-free animals for tissue donation would appear prudent. Thus, encompassed within the present invention is a method of screening potential organs donors for TTV using an assay similar to that described in detail in Example 7. Animals that test positive for genomic TTV sequences in their serum or plasma could then be rejected as possible donors, if appropriate.

The present invention will now be described by way of examples, which are meant to illustrate, but not to limit, the spirit and scope of the invention.

EXAMPLES

Example 1. Transmission of TTV to non-human primates.

Several studies have observed a high prevalence of TTV in individuals at risk for infection with parenterally transmitted viruses, suggesting that TT virus can be transmitted by blood and/or blood products. However, there have been no cases of TTV transmission reported in the literature to date. To investigate whether TTV is a transmissible agent, and if it can be transmitted parenterally, serum or plasma from two chronic nonA-GBV-C hepatitis patients known to be infected with TTV were intravenously inoculated into chimpanzees.

Non-human primate transmission studies were conducted at the Southwest Foundation for Biomedical Research in San Antonio, Texas. All animals were maintained and monitored according to protocols that met all relevant requirements for the humane care and ethical use of primates in an approved facility. Baseline serum levels were established for the liver-specific enzymes alanine aminotransferase (ALT), gamma-glutamyltransferase (GGT) and aspartate aminotransferase (AST). Animals were inoculated intravenously with TTV-containing human serum or plasma from individuals diagnosed with chronic nonA-E hepatitis and then monitored twice weekly for serum levels of the above liver-specific enzymes. Chimpanzee 314 (CH314) was inoculated with 20 ml of human plasma

from patient A and chimpanzee 306 (CH306) was inoculated with 2.0 ml human serum from patient B.

TTV viremia was determined by nested PCR using a modified primer set orginally described by (Simmonds et al., The Lancet 352:191-194 (1998)). First round primers were A5430 (SEQ ID NO. 1) and a modified A5427 primer (SEQ ID NO. 2); second round primers were A8761 (SEQ ID NO. 3) and A5432 (SEQ ID NO. 4) was used in the first round amplification. PCR used total nucleic acids extracted from 100 µl chimpanzee serum using the QIAamp Blood Kit (QIAGEN, Chatsworth, CA) as directed by the manufacturer. Nucleic acids were ethanol precipitated and suspended in 25 µl of water. First round PCR utilized 4 µl of the extracted nucleic acids in a 20 µl reaction volume. Cycling conditions for first round (45 cycles) and second round (40 cycles) amplification were 94°C for 1 minute followed by 94°C/20 sec, 55°C/30 sec, and 72°C/30 sec; final extension at 72°C/5 min. Products were analyzed by agarose gel electrophoresis with visualization by ethidium bromide fluorescence. The approximate titers of TTV in the human inocula were determined by making serial 2-fold dilutions of extracted nucleic acids and performing PCR as described above.

Fecal material was suspended in PBS (15% w:v), vortexed and centrifuged at 3000 x g, 4°C for 10 min. The supernatant was transferred to a clean tube and centrifuged at 8000 x g at 4°C for 5 minutes. Nucleic acids were extracted from 200 µl of the resulting supernatant using the QIAamp Blood Kit. Nucleic acids were ethanol precipitated and resuspended in 15 µl water. TTV PCR was performed as described above.

Twenty ml of plasma from one patient (approximate TTV titer: 2 x 10^3 genome copies/ml) was inoculated into chimpanzee 314 (CH314). Two ml of serum from a second patient (approximate TTV titer: 1 x 10^3 genome copies/ml) was inoculated into chimpanzee 306 (CH306). TTV DNA was detected in CH314 serum for 28 days starting 93 days post-inoculation (PI, Table 1).

Table 1. Presence of TTV in chimpanzee serum

CHIMP 314		CHIMP 306	
Weeks Post-Inoculation	TTV PCR	Weeks Post-Inoculation	TTV PCR
-0.7	-	-0.2	-
1	-	1	-
2	-	2	-
3	-	3.3	-
5	-	4.3	-
7	-	6	-
9.3	-	8.3	-
10.3	-	10.3	-
13.3	+	12.3	-
15.3	+	19	-
17.3	+	21	-
32.3	-	21.3	+
33.3	-	22	+
34.3	-	23	+
		25	+
		26.3	+
		27.3	+
		28	+
		29	+
		30	+
		31	+

The duration of the viremia is unclear because samples between 121 and 226 days PI were not available. However, sera collected later than 226 days were negative. TTV DNA was detected in CH306 serum starting at 149 days PI and remained positive until 219 days PI, at which time viral DNA became undetectable. The later appearance of TTV viremia in CH306, compared to CH314 (149 vs. 93 days PI), may be due to the lower volume and titer of the inoculum used. Nucleic acids extracted from CH306 fecal samples spanning 133-175 days post-inoculation were tested for TTV via nested PCR, however TTV DNA was not detected. Thus, TTV is either (a) not shed in the feces of CH306, or (b) not present in the feces during the time frame tested, or (c) below the limit of detection. TTV sequences present in the human inocula and in the corresponding chimpanzee recipients were found to be 100% identical, while the sequences of the TTV PCR products from the two human inocula were only 91% identical (data not shown). The complete conservation of TTV sequences between source and recipient indicates that TTV infection was derived from its corresponding inoculum, thus demonstrating the infectious nature of the inoculum and the parenteral transmissibility of the virus. Neither chimpanzee exhibited any biochemical or histologic evidence of hepatitis.

Example 2. Biophysical Characterization of TTV

In an effort to further characterize TT virus, the studies of Nishizawa et al. and Okamoto et al. (Nishizawa et al., Biochem Biophys Res Commun 241:92-97 (1997); Okamoto et al., Hepatol. Res. 10:1-16 (1998)) were extended and repeated through biophysical characterization of the virus. The present data

confirm the single-strandedness of the DNA genome and strongly suggest that it is circular and not linear as previously believed. In addition, nuclease protection assays using strand-specific probes suggests that TTV possesses a negative-stranded genome.

Example 2.1 Estimation of TTV particle size. Filtration studies to determine the approximate size of the putative virion utilized 50 μl of TTV positive serum combined with parvovirus B19-containing human serum (10^6 virus particles). The sample was diluted to 1.0 ml with phosphate buffered saline (PBS) and spun for 10 min at 12,000 x g and 4°C. The supernatant was passed sequentially through 13 mm polycarbonate filters (Costar) with decreasing pore sizes of 200 nm, 100 nm, 50 nm, 30 nm and 15 nm. PBS (100 μl) containing 0.1 mg/ml bovine serum albumin was passed through all filters prior to use. Aliquots (100 μl) of unfiltered serum and the resulting filtrates were extracted for total nucleic acid using the DNA/RNA Isolation Kit (Amersham Life Science Inc., Arlington Heights, IL) as directed by the manufacturer. TTV and B19 sequences were detected by PCR (20 μl final reaction volume) by using AmpliTaq Gold DNA polymerase (Perkin Elmer, Foster City, CA) and 2μl (20%) of each extracted sample. TTV primers were as described in Example 1 (SEQ ID NOS. 7 and 8). Parvovirus B19 primers were: B19-forward (SEQ ID NO. 9) and B19-reverse (SEQ ID NO. 10). Reactions were heated 8 min at 94°C followed by 40 cycles of 94°C/20 sec, 55°C/30 sec and 72°C/30 sec, followed by 3 min final extension at 72°C. Second round of amplification was performed as described above using an aliquot of the first round

products and either the same primers (B19, SEQ ID NOS. 5 and 6) or nested primers (TTV, SEQ ID NOS. 3 and 4). Products were analyzed by agarose gel electrophoresis with visualization by ethidium bromide fluorescence.

As expected, parvovirus B19 particles (a nonenveloped, single-stranded DNA virus with a reported diameter of 18 nm to 22 nm) was detected in the 200 nm, 100 nm, 50 nm and 30nm filtrates, but not in the 15 nm filtrate. TTV was detected in the 200 nm, 100 nm, and 50 nm filtrates but not in the 30 nm or 15 nm filtrates. Thus, TTV virions appear to exist in serum with a particle diameter between 30 and 50 nm.

Example 2.2 Determination of TTV buoyant density. Human sera containing TT virus (200 µl) or parvovirus B19 (20 µl, approximately 2 ng B19 DNA) were mixed and centrifuged at 14,000 x g for 15 minutes at 4°C. Supernatants were combined and mixed with 11.5 ml CsCl (1.302 g/ml). Isopycnic gradients were formed by centrifugation in a Beckman SW41Ti rotor at 35,000 rpm (150,000 x g) for 65 hours at 6°C. Fractions (≈800 µl) were collected from the bottom of each gradient, refractive indices were measured to determine the density, and 200 µl of each fraction was extracted for total nucleic acids using the High Pure Viral RNA kit (Boehringer Mannheim, Indianapolis, ID). One-tenth of the isolated nucleic acid was tested for TTV or B19 by PCR using AmpliTaq Gold (Perkin Elmer, Foster City, CA) as directed by the manufacturer. PCR reactions (20 µl) utilized 1 µM primers (TTV: SEQ ID NOS. 7 and 8, B19: SEQ ID NOS. 9 and 10). Reactions were thermocycled (94°C, 9 min; 40 cycles of 94°C/20

sec, 55°C/30 sec, 72°C/30 sec; final extension at 72°C/10 min) and 10 µl from each reaction were separated by agarose gel electrophoresis, capillary transferred to Hybond-N+ (Amersham, Arlington Heights, IL), and visualized via Southern hybridization using an amplicon-specific ^{32}P-labeled DNA probe.

PCR analysis of the gradient fractions located TTV in fractions with a density of 1.31 - 1.34 g/ml (data not shown). This is similar to the CsCl buoyant density reported by Okamoto et al. (Okamoto et al., Hepatol. Res. 10:1-16 (1998)). In contrast, parvovirus B19 was found in fractions with a density of 1.38 - 1.51 g/ml (data not shown). Thus, TTV possesses a buoyant density significantly lighter than parvovirus B19.

Example 2.3 Demonstration of the single-stranded nature of the TTV genome. To investigate whether the TTV genome was single or double stranded, serum nucleic acids obtained using the DNA/RNA Isolation Kit (USB) were treated with Mung Bean Nuclease (NEB, Beverly, MA) at a final concentration of 1.0 U/µl for 30 minutes at 30°C (10 µl volume). Ten microliters of 50 mM Tris (pH 8.9) was added and the samples heated to 99°C for 5 minutes. Samples were then diluted to 100 µl with PCR reaction mix to achieve 1X concentration and amplified for 35 cycles (95°C, 20 seconds; 55°C, 30 seconds; 72°C, 30 seconds) with TTV-specific primers (SEQ ID NOS. 11 and 12). Heminested PCR reactions were then performed using 5 µl of the first round product with SEQ ID NOS. 13 and 12. Both TTV positive and negative serum samples were tested, and the experiment was controlled by using a double-

stranded plasmid (pGEM-T EASY, Promega, Madison, WI) containing a 1.3 kbp insert derived from TTV and a single-stranded phagmid of the same plasmid. Phagmid were produced as described (Sambrook et al., (1989)) using R408 helper phage (Stratagene, La Jolla, CA). Single-stranded phagmid DNA was isolated with the QIAquick Spin M13 kit (Qiagen, Chatsworth, CA) and quantitated by UV absorbance.

PCR amplification of these nucleic acids revealed the presence of the viral DNA prior to, but not following digestion with MBN (Figure 1). Under the same reaction conditions, double-stranded plasmid DNA containing a 1.3 kbp fragment of the TTV genome was resistant to MBN digestion, while single-stranded phagmid DNA derived from the same plasmid was not. This result indicates that the genome of TT virus is single-stranded, at least within the region amplified by the primers used to detect the virus in these experiments.

Example 2.4 Determination of TTV Genome Polarity. To establish the polarity of the TTV genome, a hybridization/nuclease protection assay was performed using serum total nucleic acids containing TTV DNA and strand-specific RNA run-off transcripts made from plasmids containing identical TTV sequences, but in opposite orientations. Reduction of template plasmid DNA concentration to below detectable limits was achieved by repeated digestion with DNAse I and organic extraction with TRIzol reagent (GibcoBRL, Gaithersburg, MD). Control experiments used plus or minus strand, single-strand phagemid DNA made from the same plasmids.

Total nucleic acid was extracted as above from TTV-positive human serum (100 µl) with a sequence identical to that of the cloned TTV sequence over the region to be analyzed, and resuspended in 40 µl of water. Plus or minus strand RNA transcripts (2 ng, 10^{10} copies) were mixed, in separate reactions, with (a) plus or minus strand phagemid DNA (300 copies), (b) 10 µl of the extracted nucleic acids, and (c) water without DNA. The samples were dried under vacuum, dissolved in 8 µl of 30 mM EPPS, pH 8.1 containing 3 mM EDTA, overlaid with mineral oil and heated for 3 minutes at 99°C. After adding 2 µl of NaCl (5M), the samples were hybridized at 67°C for 21 hours. One half (5 µl) of each hybridization was added to 45 µl buffer (33.3 mM sodium acetate, pH 5.2; 1.44 mM $ZnSO_4$; 5.5% glycerol), with or without Mung Bean Nuclease (6 Units/reaction), and incubated 30 minutes at 30°C. The nuclease was inactivated by adding 6 µl of 467 mM Tris-HCl, pH 8.9; 14 mM EDTA and heating 5 minutes at 99°C. Nucleic acid was ethanol precipitated and resuspended in 20 µl water. Four microliters of each sample was tested for the presence of TTV sequences by nested PCR (20 µl) followed by agarose gel electrophoresis as described above. The first round primers were A8761 (SEQ ID NO. 3) and A1 (SEQ ID NO. 14); second round primers were S2 (SEQ ID NO. 15) and A2 (SEQ ID NO. 16). These primers are specific for, and contained within, the cloned TTV region from which run-off transcripts and phagemid were made.

In the absence of nuclease, TTV was always detected except in the RNA-only hybridizations (Table 2). In the presence of nuclease, however, TTV viral

DNA was detected only in hybridizations containing plus-strand RNA. The TTV-containing phagemid DNA controls were detected only when the hybridizations contained the opposite strand RNA. These results strongly suggest that TTV is a negative-stranded DNA virus.

Table 2.

Hybridization[a]		PCR Detection of TTV	
RNA	DNA	Without MBN[c]	With MBN
Plus[b]	Plus	+	-
Plus	Minus	+	+
Plus	TTV	+	+
Plus	None	-	-
Minus	Plus	+	+
Minus	Minus	+	-
Minus	TTV	+	-
Minus	None	-	-

[a]Nucleic acids present in the hybridization

[b]The strand polarity of the nucleic acid, plus or minus

[c]Treatment of the hybridization with or without Mung Bean Nuclease (MBN)

Example 3. Genomic Extension and Demonstration of the Circular Nature of TTV.

To obtain the genomic sequence, total nucleic acids were extracted from a West African individual (GH1) using the DNA/RNA Isolation Kit (Amersham Life Science Inc., Arlington Heights, IL) as recommended by the manufacturer. Initial anchored PCR extension products were generated up- and down-stream of the N22 clone region (Nishizawa et al., Biochem Biophys Res Commun 241:92-97 (1997)) by anchored PCR (Sorensen et al., J. of Virol. 67:7118-7124 (1993); Leary et al.,

J. of Med. Virol. 48:60-67 (1996)). The TTV-specific primers used to obtain sequences upstream of the N22 region were: N22-A1 (SEQ ID NO. 17) and N22-A2 (SEQ ID NO. 18). The anchored primers used to obtain sequences downstream of the N22 region were: N22-S1 (SEQ ID NO. 19) and N22-S2 (SEQ ID NO. 20). To test the possibility that the TTV genome is circular, inverted PCR using nested primers derived from the anchored PCR products was performed with Takara LA TAQ (PanVera Corporation, Madison, WI) as described by the manufacturer using the following primers: UFGH1-A1 (SEQ ID NO. 21), UFGH1-A2 (SEQ ID NO. 22), DFGH1-S1 (SEQ ID NO. 23), and DFGH1-S2 (SEQ ID NO. 24). The circular nature of the virus was confirmed by nested genome-length PCR using primers derived from the N22 region and Takara LA TAQ (first round, UFTTV1: SEQ ID NO. 25 and DFTTV1: SEQ ID NO. 26; second round, UFTTV2: SEQ ID NO.27 and DFTTV2: SEQ ID NO. 28). All PCR products were cloned into pGEM-T EASY vector (Promega, Madison, WI) and 2-4 clones sequenced. Sequencing reactions were performed with ABI Big Dye or Prism dGTP Big Dye (Applied Biosystems-Perkin-Elmer, Foster City, CA). Reactions were electrophoresed under denaturing conditions and sequence data collected on the Applied Biosystems 377 DNA Automated Sequencer as directed by the manufacturer. Sequences were compiled and edited using Sequencher version 3.0 (Gene Codes Corp., Ann Arbor, MI) and analyzed using the programs of the Wisconsin Sequence Analysis Package, version 9.0. The genomic sequence TTV-GH1 is SEQ ID NO. 29.

To obtain genome length sequence of TTV, anchored PCR was performed on nucleic acids extracted from the serum of the West African individual (GH1). Amplified

genome fragments were generated upstream (1766 bp) and downstream (882 bp) from the N22 region of TTV-TA278 (Nishizawa et al., Biochem Biophys Res Commun 241:92-97 (1997)). Assuming that the TTV genome was circular, inverted PCR utilizing upstream anti-sense primers and downstream sense primers was performed, generating a 1300 bp product representing the remainder of the genome. The circular structure of the viral genome was reproducibly confirmed by nested genome-length PCR originating from the N22 region that produced the expected product of approximately 3700 bp. The genomic sequence of this isolate (designated GH1) comprises 3852 nucleotides (Fig. 2), 113 nucleotides longer than that of TTV-TA278 (Okamoto et al., Hepatol. Res. 10:1-16 (1998)). This additional sequence, located at the extreme 3'-end of the linear TA278 sequence (positions 3740-3852, SEQ ID NO. 29), consists of 89% G or C residues and possesses multiple inverted repeats. Alignment of TTV-GH1 and TTV-TA278 reveals 93% identity across the entire genome. The region with the lowest degree of conservation lies between bases 1440-1827, SEQ ID NO. 29 and exhibits only 73.6% identity. The region of highest identity lies between bases 2240-2911, SEQ ID NO. 29, exhibiting 99.5% identity. Both TTV-TA278 (Okamoto et al., Hepatol. Res. 10:1-16 (1998)) (GenBank accession no. AB008394) and TTV-GH1 (SEQ ID NO. 29) encode two large open reading frames of 203 (SEQ ID NO. 30) and 770 amino acids (SEQ ID NO. 31) (Fig. 2) exhibiting 95 and 96% identity between the isolates. The ORF1 protein of both isolates possesses an arginine-rich region at its amino terminus (44 of first 82 amino acids, SEQ ID NO. 31). The ORF1 regions from amino acids 1-274 exhibit 100% identity, but positions 275-

405 exhibit only 69% identity. The remainder of the ORF1 protein is 100% conserved between the two isolates. No significant identity with non-TTV sequences was obtained upon BLAST analysis of TTV-GH1 against the GenBank or SWISPROT databases.

Previous interpretation of biophysical and molecular data suggested that TT virus resembled members of the *Parvoviridae* (Okamoto et al., J. of Med. Virol. 56:128-132 (1998); Okamoto et al., Hepatol. Res. 10:1-16 (1998)). In Example 2, we confirmed that TTV possesses a single-stranded DNA genome, consistent with the *Parvoviridae*. However, the buoyant density in CsCl of TT virus (1.31-1.34 g/cm^3) and its particle size determined by filtration (30-50 nm) are not like other parvoviruses (1.39-1.42 g/cm^3 and 18-22 nm). Most notably, the TT virus genome was found to be circular, not linear as previously reported (Okamoto et al., Hepatol. Res. 10:1-16 (1998)). This was demonstrated using inverse PCR and primers located at the termini of anchored PCR products located up- and downstream of the original N22 sequence to generate an amplicon of about 1300 bp (Fig. 2). Had the genome been linear, no amplicon would have been produced. Furthermore, inverse PCR using primers derived from the N22 region were able to produce a 3700 bp product encompassing nearly the entire genome, including those sequences originally believed to be at the 5' and 3' termini. Similar products have been generated from several other TTV positive samples (data not shown). The genome sequence of this TTV isolate, designated GH1 (SEQ ID NO. 29), was found to be 3852 nucleotides in length, 113 nucleotides longer than previously reported (Okamoto et al., Hepatol. Res. 10:1-16 (1998)). The

newly discovered region is GC rich (89%) and contains several potential stem-loop structures. Amplification of this region was possible only when contained within PCR products greater than 700 bp. These findings may explain the failure of previous attempts to demonstrate the circular nature of the genome that used inverse PCR with primers located near the presumed termini (Okamoto et al., Hepatol. Res. 10:1-16 (1998)).

Other than its single-stranded genome and lack of an envelope, TTV does not share any other characteristics of the *Parvoviridae*. TT virus does share some attributes of the *Circoviridae*. Members of this family include chicken anemia virus (CAV), psittacine beak and feather disease virus and porcine circovirus (PCV) (Lukert et al., Virus Taxonomy: The Classification and Nomenclature of Viruses. The Sixth Report of the International Committee on Taxonomy of Viruses (1995)). Circoviruses are nonenveloped, 15-22nm in diameter, and band in CsCl at 1.33-1.37 g/ml. Their genomes comprise a single molecule of circular, single-stranded DNA 1.7-2.3 kb in length and with either positive or ambisense polarity (Lukert et al., Virus Taxonomy: The Classification and Nomenclature of Viruses. The Sixth Report of the International Committee on Taxonomy of Viruses (1995; Niagro et al., Archives of Virology 143:1723-1744 (1998)). The TT virus genome is nearly 4 kbp in length and, based upon nuclease/hybridization protection assays, appears to encapsidate the negative-strand, with respect to the ORF1 gene encoded on the complementary, or positive strand (Fig. 2). Though the particle size and circular DNA genome of TTV are larger than that reported for the *Circoviridae*, TT virus and circoviruses possess

similar densities in CsCl, suggesting a similar protein to DNA ratio.

Nucleotide and amino acid sequence database searches failed to identify significant sequence similarity between TTV-GH1 and other viruses as has been reported previously (Okamoto et al., Hepatol. Res. 10:1-16 (1998)). The similarities in genome structure and composition between TTV and the *Circoviridae* prompted a more detailed comparison. Circoviruses contain stem-loop structures essential for DNA replication in which the loop possesses a nonanucleotide motif conserved among plant and animal circoviruses. However, CAV is an exception in that the nonanucleotide motif is semi-conserved but is not associated with a stem-loop structure (Niagro et al., Archives of Virology 143:1723-1744 (1998)). This motif was not identified in TT virus. In TTV, the three largest stem-loop structures identified lie outside the ORF1 and ORF2 coding regions and two of these stem-loops are located within the 113 nucleotide region cloned from TTV-GH1.

TTV encodes two large (203 and 770 amino acids, SEQ ID NOS. 30 and 31, respectively) and several small ORFs (33-105 amino acids). The circoviruses encode up to seven ORFs (Bassami et al., Virology 249:435-459 (1998)), including the Rep protein, involved in rolling circle replication (Niagro et al., Archives of Virology 143:1723-1744 (1998)). The Rep protein possesses up to four amino acid sequence motifs conserved among many plant and animal circoviruses and bacteriophage ΦX-174 (Niagro et al., Archives of Virology 143:1723-1744 (1998)). Conserved motifs 1 (FTL) and 3 (YXXK) were identified in ORF1 of TTV-GH1. The active site tyrosine in motif 3 was conserved in

the ORF1 proteins of TTV-GH1 and TTV-TA278. Motif 4, or the P-loop (putative ATP/GTP binding motif), was not found. This motif is also absent in the putative Rep protein (encoded by ORF1) of CAV. The capsid or coat proteins of most circoviruses are encoded by separate genes and are highly basic (rich in arginine or lysine) (Niagro et al., Archives of Virology 143:1723-1744 (1998)). CAV is the exception, however, in that its ORF1 protein contains a highly basic amino-terminus and also possesses three of the four conserved Rep protein motifs closer to the carboxyl-end. ORF1 of TTV encodes 44 arginine residues of the first 100 amino acids and, towards the carboxyl-end of ORF1, possesses two of the four conserved Rep protein motifs. Thus, TTV ORF1 appears to resemble the CAV ORF1 protein (Niagro et al., Archives of Virology 143:1723-1744 (1998)) and the presence of these conserved features in TTV ORF1 suggests that TTV may replicate by a rolling circle mechanism. However, until viral transcripts and their encoded gene products are identified, the actual coding regions of TTV and their function will be difficult to determine with certainty.

From the data presented here and in Example 2 (above), it is clear that TT virus cannot be classified within an existing virus family. The circular nature of the genomic DNA, in addition to the virion size, buoyant density and lack of sequence identity preclude its membership among the *Parvoviridae*. However, by virtue of its negative-stranded, circular DNA genome, TT virus is most closely related to the *Circoviridae*, although TTV possesses a larger genome and viral particle relative to members of this family. Furthermore, the absence of

significant sequence similarities between TTV and circoviruses, beyond the possible conservation of motifs involved in rolling circle replication, do not support inclusion of TTV in the *Circoviridae*. Therefore, it is proposed that TTV is a member of a new virus family that infects humans, tentatively named the *Circinoviridae*, derived from the Latin *circinatio* meaning 'the describing of a circle'.

Example 4. Dectection of TTV with Published Primer Sets

Serum panels from a broad spectrum of diseased and normal individuals were studied for TTV presence. These included normal volunteer donors (Southeastern Wisconsin, USA), commercial blood donors (Central and Southern USA), intravenous drug abusers (IVDA; Chicago, Illinois, USA), blood donors with elevated serum alanine aminotransferase levels (Eastern USA), hemophiliacs (Netherlands), and randomly selected Japanese sera, some of which were seropositive for HTLV-I. Additionally, sera from Ghanaian children (Martinson et al., J. of Med. Virol. 48:278-283 (1996)) and individuals diagnosed with non-A-E hepatitis (Dawson et al., J. of Med. Virol. 50:97-103 (1996); Rochling et al., Hepatology 25:478-483 (1997)) were tested.

Detection of TTV DNA sequences by PCR. Total nucleic acids were extracted from 25 µl of serum using the DNA/RNA Extraction kit (Amersham Life Science Inc., Arlington Heights, IL). Nucleic acids were dissolved in 25 µl of nuclease-free water and 4 µl used as template in the amplification reactions. Oligonucleotide primers used were those described by Nishizawa (Nishizawa et al., Biochem Biophys Res

Commun 241:92-97 (1997)) (RD037 and RD038, SEQ ID NOS. 32 and 33, respectively) followed by RD051 and RD052, SEQ ID NOS. 34 and 35, respectively) or Simmonds (Simmonds et al., The Lancet 352:191-194 (1998)) (SEQ ID NOS. 1 and 2 followed by SEQ ID NOS. 3 and 4), hereinafter referred to as "Set 1" or "Set 2", respectively.

Amplification reactions (20 µl) were performed for thirty-five cycles (94°C for 20 seconds, 55°C for 30 seconds, and 72°C for 30 seconds) and contained 1.0 µM final concentration each primer and 1.5 units of Taq DNA polymerase (Perkin-Elmer, Foster City, CA). Nested PCR reactions were performed on 1.0 µl of the primary PCR reaction using the same amplification conditions as above. PCR products were analyzed by 2% agarose gel electrophoresis with visualization via ethidium bromide fluorescence. The identity of the amplified product was confirmed by Southern hybridization to sequence confirmed probe (nested or heminested PCR product).

Results. TTV viremia was detected in approximately 10% of volunteer donors in the United States with or without elevated transaminase levels (Table 3), and was slightly more prevalent in commercial blood donors (13%).

Table 3. Prevalence of TTV in Blood Donors

Group	No. Positive	Percent Positive
Volunteer Donors (High ALT) (n=165)	15	9.1%
Volunteer Donors (n= 150)	16	10.7%
Commercial Donors (n=148)	19	12.8%

HCV NS5-only positive Donors, US (n=41)	2	4.9%
Japanese Individuals (n=61)	32	52.5%

In a small panel of volunteer donors previously shown to have antibodies only to the NS5 antigen of HCV (Leary et al., Journal of Virological Methods 56:119-121 (1996)), approximately 5% were TTV DNA positive. Thus, the overall prevalence rate among US blood donors was 10.3%. These results differ from recently reported prevalence rates of 1.9% (19 of 1000) and 1% (1 of 100) in normal blood donors from the UK and the US, respectively (Charlton et al., Hepatology 28:839-842 (1998; Simmonds et al., The Lancet 352:191-194 (1998)). However, Nauomov et al., (Naoumov et al., The Lancet 352:195-197 (1998)) reported a rate of 10% (3 of 30) in UK normal blood donors. Each of these studies utilized different nucleic acid extraction methods as well as PCR conditions and primers. In addition, Southern hybridization was not performed to possibly identify positive samples not visualized via ethidium bromide fluorescence; thus, the true prevalence may have been underestimated. Although each sample in the current study was tested with two distinct primer sets, not all positive samples were identified by primer set 2 (Table 4).

Table 4. Number of samples testing positive for TTV DNA:

Comparison of two PCR primer sets

Group	Set 1 Only	Set 2 Only	Both Sets	Tota 1
Volunteer Donors (High ALT)	6	7	2	15

(n=165)				
Volunteer Donors (n= 150)	3	9	4	16
Commercial Donors (n=148)	1	13	5	19
IVDA (n=87)	0	7	8	15
Hemophiliacs (n=169)	1	80	14	95
TOTAL	11	116	33	160

Set 2 detected more samples within each group, but primer set 1 detected additional samples that were negative with set 2 primers. Set 1 alone underestimated the prevalence of TTV infection by 200-600%, while set 2 alone underestimated the prevalence by 1-40%. These data clearly indicate that while PCR primer set 2 possesses superior sensitivity, it does not identify all TTV DNA positive sera. This result, combined with the observation that TTV DNA sequences demonstrate as much as 40% divergence, suggests that studies utilizing the currently described primer sets may significantly underestimate the true prevalence of TTV. These results also illustrate the need to develop optimal oligonucleotide primers in order to detect all TTV variants. Full length genomic sequences from multiple variants are required for the identification of conserved regions for optimal primer design.

Sera from individuals considered to be "at risk" for acquiring parenterally transmitted viral agents were also tested. TTV DNA was found in 17% (15/87) of intravenous drug abusers in the USA and 56% (95/169) of hemophiliacs from the Netherlands (Table 5).

Table 5. Prevalence of TTV in At-Risk Individuals

Group	No. Positive	Percent Positive
IVDAs, USA (n=87)	15	17.2%
Hemophiliacs, Netherlands (n=169)	95	56.2%
Ghana, West Africa (n=24)	14	58.3%
Non-A-E Hepatitis, USA (n=48)	1	2.1%

In contrast, patients diagnosed with non-A-E hepatitis revealed very low prevalence in US patients (2.1%). The reason for the discrepancy between the TTV infection rate among blood donors (Table 3) and non-A-E hepatitis patients in the US is unclear, though it may reflect the small sample size of the non-A-E hepatitis patients. However, the high rate of infection among IVDAs and hemophiliacs indicates an association between increased infection risk and high rates of exposure to blood or blood products.

Among randomly selected Japanese sera tested, 32 of 61 (52%) were found to be TTV positive. This rate is higher than originally reported for blood donors in Japan (Okamoto et al., Hepatol. Res. 10:1-16 (1998)), however, this panel included some individuals who were HTLV-I positive, and thus, may be at higher risk for infection with blood-borne viruses. Among Ghanaian children ages 6-18, TTV was detected in 58% of individuals tested (Table 5). This group has very low rates of parenteral exposure, no history of tattooing, ear piercing, or needle sharing during vaccination, and are not sexually active. This population exhibited an overall seroprevalence rate of 61% for at least one marker of HBV infection, 16% for HBsAg, 5.4%

for HCV (Martinson et al., J. of Med. Virol. 48:278-283 (1996)), and 15% GBV-C RNA (Dawson et al., J. of Med. Virol. 50:97-103 (1996)). The relatively high rate of TTV infection in Ghana, compared to that of HCV or GBV-C, may indicate that TTV is more virulent upon parenteral exposure (similar to HBV) or that TTV is also transmitted by other means.

The occurrence of GBV-C and TTV coinfection in commercial blood donors and intravenous drug abusers (IVDAs) is quite low at 0.7-3.6%, despite nearly equivalent infection rates for the two viruses in these populations, i.e. 13-18% (Table 6).

Table 6. TTV and GBV-C coinfection rates in various populations.

	TTV DNA+	GBV-C RNA+	GBVC+ and TTV+
Volunteer Donors (n=99)	14 (14%)	2 (2.0%)	1 (1.0%)
Commercial Donors (n=148)	19 (13%)	22 (15%)	1 (0.7%)
IVDA (n=84)	15 (18%)	12 (14%)	3 (3.6%)

This suggests that GBV-C and TTV infection may occur via different transmission routes. While GBV-C has been shown to be exclusively transmitted parenterally (Dawson et al., J. of Med. Virol. 50:97-103 (1996)), it is possible that TTV infection occurs through exposure to infected blood or blood products and may also be community acquired, i.e. transmitted via the fecal-oral route. This mode of transmission could explain the relatively high prevalence of TTV infection in Japan ((Okamoto et al., Hepatol. Res.

10:1-16 (1998)), and this study), the US and Ghana (Tables 3 and 5). Indeed, TTV viremia in underdeveloped nations has been shown to be 7-74% in the indigenous rural people of Nigeria, Gambia, Brazil, and Ecuador (Prescott and Simmonds, New England Journal of Medicine 339:777 (1998)) and a recent study has demonstrated the presence of TTV DNA in human fecal material (Okamoto et al., J. of Med. Virol. 56:128-132 (1998)). Thus, the very high incidence of TTV infection in developing regions may be due to poor sanitary conditions resulting in the fecal-oral transmission of the agent.

The causal role of TTV in hepatitis is questionable given the low prevalence among non-A-E hepatitis patients and the relatively high rate in volunteer donors with or without elevated transaminase levels. The association between TTV infection and post-transfusion hepatitis indicated by Nishizawa et al (Nishizawa et al., Biochem Biophys Res Commun 241:92-97 (1997)) was concluded from the presence of TTV viremia in 3 of 5 selected patients who exhibited elevated transaminase levels following transfusion. It should be noted that these patients did not have clinically apparent hepatitis and that TTV was found in two of three patients diagnosed with carcinoma of the esophagus or gall bladder. Thus, while current studies of populations from developed countries (i.e. US, UK, and Japan) have demonstrated that TTV prevalence is higher in individuals at risk for acquiring parenterally transmitted diseases (Charlton et al., Hepatology 28:839-842 (1998); Okamoto et al., Hepatol. Res. 10:1-16 (1998); Simmonds et al., The Lancet 352:191-194 (1998)), its association with

disease, especially post-transfusion hepatitis, is questionable.

Based upon the data presented, it is apparent that the primers currently in use do not detect all viremic samples and, as a result, underestimate the true prevalence of TT virus infection. The cloning and sequencing of TTV genomes from around the world will allow the identification of conserved regions from which universal PCR primers can be designed as has been done for HCV (Bukh et al., Proc. Natl. Acad. Sci. USA 89:187-191 (1992)) and GBV-C (Leary et al., J. of Virol. Methods 56:119-121 (1996); Muerhoff et al., J. of Virol. Methods 62:55-62 (1996)). Such studies will further our understanding of the genomic organization of the virus and lead to the elucidation of its encoded proteins. The identification of immunogenic proteins is necessary for the development of serologic screening assays for TTV detection, thereby providing another tool for examination of the natural history of TTV infection, its epidemiology and disease association, if any.

Example 5. Phylogenetic Analysis of TTV sequences.

To determine the degree of sequence variability of TTV we examined a 260 bp region of the genome (not including primer sequences used during PCR) amplified from 151 globally distributed individuals. PCR products were generated using primers described in Example 1 by a hemi-nested PCR method: primers A5430 and A5427m (SEQ ID NOS. 1 and 2) were used for first round amplification followed by A8761 and A5427m (SEQ ID NOS. 3 and 2) for second round amplification, using the cycling method described in Example 4 (above). Products were separated by agarose gel electrophoresis

and gel purified using the Qiaex II Gel Extraction Kit (Qiagen, Chatsworth, CA). Purified products were sequenced directly. Those products which yielded uninterpretable sequence (significant degree of ambiguities) were cloned into pGEM-T EASY (Promega, Madison, WI) and at least six clones of each PCR product were sequenced.

The TTV sequences determined in this study and those deposited in GenBank that overlapped the amplified region were aligned using the program PILEUP (Wisconsin Package, version 9.0). PCR primer sequences were not included in the sequence alignment. The final alignment of 163 sequences (260 nucleotides in length) was utilized to determine the evolutionary relationship between isolates by using the programs of the PHYLIP package, version 3.5c (Felsenstein, (1993)). Nucleotide sequence distances were determined using DNADIST. Amino acid sequence distances were determined using PROTDIST; calculated distances were then used by NEIGHBOR to generate unrooted trees. The program RETREE with the midpoint rooting option was used to plot the trees. Bootstrap values were determined on 100 resamplings of amino acid sequences and 1000 resamplings of nucleotide sequences using SEQBOOT, DNADIST for nucleotide sequences or PROTDIST for amino acid sequences, NEIGHBOR, and finally CONSENSE to generate the majority rule consensus tree. Bootstrap values greater than 70% were considered supportive of the observed groupings. The final trees were visualized with TREEVIEW (Page, Computer Applications in the Biosciences 12:357 (1996)).

Of the 151 PCR products sequenced, 54 yielded over 10% nucleotide sequence ambiguities, suggesting

the presence of mixed infections. This was confirmed by cloning and sequencing of 12 of 54 products which revealed up to 36% DNA sequence variability between sequences cloned from a single individual. The sequences we determined were aligned with 36 TTV sequences obtained from GenBank, including representatives of the putative genotypes (1a, 1b, 2a, 2b) previously characterized (Okamoto et al., Hepatol. Res. 10:1-16 (1998); Simmonds et al., The Lancet 352:191-194 (1998)). The pairwise genetic distances calculated for all 163 aligned sequences clearly shows two tiers of sequence diversity (Figure 3), suggesting the existence of distinct genetic groups or genotypes. There was a high degree of variability, up to 0.62 substitutions per position, (or an uncorrected distance of 44%) within this putative coding region of the virus. In general, pairwise distances lower than 0.26 represent intragroup distances and values higher than 0.34 represent intergroup distances.

These pairwise distances were used to generate an unrooted phylogenetic tree (Figure 4). Three major groups were observed with approximately equally divergence from each other. These major groups were strongly supported by bootstrap analysis: groups 1 or 3 sequences associated in 100% of the trees while group 2 sequences grouped in 85% of the trees. Although subgroups 1a and 1b have been described previously (Okamoto et al., Hepatol. Res. 10:1-16 (1998; Simmonds et al., The Lancet 352:191-194 (1998)), and the branching order of group 1 sequences suggests the presence of two subgroups, the associated bootstrap values are less than 44%. Thus, we found no support for group 1 subtypes. Based upon pairwise

distances, the two sequences constituting subtype 2.2 (Figure 4), both from Japan, are more closely related to subtype 2.1 isolates than those in groups 1 or 3 (table 7); and thus have been segregated into a group 2 subtype rather into their own major group.

Table 7. Phylogenetic Distances DNA Distances

			1	2.1	2.2	3
1	0-0.18		0-0.18	0.41-0.62	0.42-0.52	0.39-0.55
2.1	0.46-0.61	0-0.17		0-0.23	0.26-0.36	0.34-0.54
2.2	0.35-0.48	0.16-0.25	0.06		0.03	0.36-0.47
3	0.43-0.63	0.33-0.52	0.34-0.41	0-0.22		0.02-0.26
	1	2	2'	3		

Amino acid sequence distances

There is strong bootstrap support for the existence of these subgroups within group 2, each with at least 85% support. Subtypes 2.1 and 2.2 do not correspond with the previously purported 2a and 2b subgroups (Okamoto et al., Hepatol. Res. 10:1-16 (1998); Simmonds et al., The Lancet 352:191-194 (1998)), the latter of which, based upon bootstrap analysis, did not segregate. Support for subgroups among genotype 3 sequences was not obtained. In addition, each of the three groups contained isolates from around the world, demonstrating no clear correlation between genotype and country of origin.

Given the high degree of nucleotide sequence variability within the TTV genome region analyzed, and inability to obtain bootstrap support for subtypes, it is possible that the true phylogenetic relationships are obscured by a high rate of synonymous

substitutions. To examine this possibility, phylogenetic analysis was performed on the deduced amino acid sequences of the TTV isolates. The segregation of amino acid sequences into three major groups was supported in 96% of the trees by bootstrap analysis (data not shown). As with nucleotide sequence analysis, there was no significant bootstrap support for group 1 or 3 subtypes, although support was obtained for two group 2 subtypes in 89% of the trees. As shown for the nucleotide sequences, pairwise amino acid sequence indicate that the two subtype 2.2 sequences are more closely related to subtype 2.1 isolates than those in groups 1 or 3 (table 7).

Phylogenetic analysis with bootstrapping provided strong support for the existence of three major groups of TTV sequences exhibiting approximately equal divergence. Others have suggested the presence of TTV subtypes (Okamoto et al., Hepatol. Res. 10:1-16 (1998); Simmonds et al., The Lancet 352:191-194 (1998)), but we did not obtain bootstrap support for segregation of the previously reported 1a and 1b sequences, or any of the other group 1 sequences we determined, into subgroups. This was also true for the purported 2a and 2b genotypes. Attempts to eliminate the potential obfuscation of subtypes due to the high rate of synonymous substitutions through analysis of only first and second codon positions or deduced amino acid sequences were not successful in obtaining support for subtypes. It remains possible, however, that the region analyzed is insufficient for subtype identification due to its short length (260 nucleotides) and/or high variability. Verification of our results will require the analysis of longer

genomic segment, or ideally, full-length genome sequences.

Sequence analysis performed on 30 cloned TTV sequences from 12 individuals demonstrated that ten individuals were infected with two different TTV genotypes and two individuals were infected with representatives of all three genotypes (Fig. 4). These mixed infections occurred in individuals at high risk for infection with parenterally transmitted viruses, such as intravenous drug users, hemophiliacs, and nonA-E hepatitis patients. In contrast, only 1 of 36 TTV positive US donors was coinfected. It remains to be determined whether this observation is due to repeated infection with variant genotypes, rapid mutation of the virus within the individual, or some other mechanism.

TTV-GH1 and TA278 are 93% identical across the entire genome, but local regions of lower or higher identity exist. These two isolates exhibit 92% identity within the 260 base region analyzed for phylogenetic relationships. Genetic divergence in this region among the globally distributed isolates examined was up to 44% at the nucleotide level and 36% at the amino acid level. This degree of variability among geographically remote isolates has not been previously observed for circoviruses. Comparison of the four CAV genome sequences present in GenBank revealed 4% maximum diversity. Analysis of eleven CAV VP1 sequences from GenBank revealed only 1.5% sequence divergence (data not shown). Similar results are obtained upon comparison of PCV sequences (Meehan et al., J. Gen. Virol. 79:2171-2179 (1998)). A recent report described a hypervariable region within ORF1 of CAV spanning 13 amino acids (up to 38% divergence)

based upon comparison of eight isolates (Renshaw et al., J. of Virol. 70:8872-8878 (1996)). In contrast, the ORF1 proteins of TTV-GH1 and TA278 exhibit 5% divergence but also contain a hypervariable region spanning 126 amino acids with 31% divergence. Thus, TTV exhibits much greater variability than CAV or PCV.

Example 6. Analysis of several full length TTV genomes

Hundreds of TT virus isolates have been identified using PCR assays which amplify less than 400 nucleotides of sequence, though only one full length (isolate GH1, 3852 nucleotides, SEQ ID NO. 29) and two near full length (isolates TA278 and TTVCHN1, 3739 nucleotides, GenBank accession nos. AB008394 and AF079173, respectively) sequences have been reported. These three sequences all represent a single and subtype of the virus (1a). To more fully understand the TT virus genome, several divergent isolates have been extended to full or near full length. These sequences reveal up to 30% nucleotide divergence, three conserved ORFs, a lack of identifiable regulatory elements, and the presence of distinct genotypes and subtypes.

Example 6.1 Genome Extensions. Previously, the present inventors described the isolation of a 260 nucleotide region from 151 globally distributed TT isolates and demonstrated the existence of at least three major virus genotypes (see Example 5). Several of the most divergent sequences from this group have been extended to genome or near genome length (Table 8).

Table 8. Full or near full length TTV genomes.

Designa-tion	SEQ ID No./ GenBank Accession No.	GENOTYPE	Genome length	ORF1	ORF2	ORF3
GH1	29	1a	3852	770	150	57
JA9	52	1a	3852	770	150	57
JA20	53	1b	3853	769	150	57
JA1	54	2	3839	767	149	57
JA4	55	2	3840	767	149	57
US32	56	2	3839	228/530	149	57
US35	57	2	3839	767	149	57
JA2B	58	3	3537*	765	151	57
JA10	59	3	3539*	765	151	57
TA278	AB008394	1a	3739*	770	150	57
TTVCHN1	AF079173	1a	3739*	770	150	57

Isolate specific nested pairs of upstream antisense and downstream sense primers were utilized in an inverted PCR assay that exploited the circular nature of the viral genome (Figure 2). Briefly, total nucleic acids were extracted from 25 µl of serum using the RNA/DNA Isolation Kit (Amersham Life Science Inc., Arlington Heights, IL) as directed by the manufacturer. Nucleic acid pellets were resuspended in 25 µl water. First round PCR reactions (20 µl volume) utilized isolate specific primers (see table 9), 4 µl of total nucleic acids and Takara LA Taq (PanVera Corporation, Madison, WI) as specified by the manufacturer.

Table 9. Primers used for the construction of full length TTV genomes

		First Round		Second Round	
Genotype	Isolates	Sense	Antisense	Sense	Antisense
1a	GH1, JA9	SEQ ID NO. 36	SEQ ID NO. 37	SEQ ID NO. 38	SEQ ID NO. 39
1b	JA20	SEQ ID NO. 36	SEQ ID NO. 40	SEQ ID NO. 38	SEQ ID NO. 39
2b	JA1, JA4, US32	SEQ ID NO. 41	SEQ ID NO. 42	SEQ ID NO. 43	SEQ ID NO. 44
2c	US35	SEQ ID NO. 45	SEQ ID NO. 42	SEQ ID NO. 46	SEQ ID NO. 47

Nested PCR reactions (100 µl) were also used to isolate specific primers, Takara LA Taq and 5 µl of the first round PCR product as template. Near full length genomes were obtained for several additional isolates using a combination of specific and consensus primers to extend 5' and 3' of the 260 base region (Figure 2 and Table 10).

Table 10. Primers used for the construction of partial TTV genomes

		Upstream product			Downstream product		
Genotype	Isolates	sense	antisense1	antisense2	sense 1	sense 2	antisense
3	JA2B, JA10	SEQ ID NO. 60	SEQ ID NO. 48	SEQ ID NO. 49	SEQ ID NO. 50	SEQ ID NO. 51	SEQ ID NO. 69

Amplification products were separated by electrophoresis through a 0.8% agarose gel, then excised and purified with Geneclean II (Bio101, Vista, CA). Purified products were ligated into pGEM-T Easy (Promega, Madison, WI) and each strand was sequenced with ABI Big Dye and analyzed on the Applied Biosystems model 377 DNA sequencer.

Analysis of the full-length genomic sequences revealed that the TT virus genome ranged from 3839 to 3853 nucleotides in length. We were unable to generate full-length genotype 3 sequences. Therefore, the partial genomic sequences of 3537 to 3539

nucleotides in length were generated. These sequences started at position 94 of the full length TT virus sequence (SEQ ID NO. 29) and ending approximately 210 bases short of the full-length sequences. BLAST searches of the GenBank database utilizing these nine distinct isolates did not reveal significant similarities to any other known sequence.

Example 6.2. Nucleotide Analysis. Nucleotide sequence comparisons were performed as described in Examples 3 and 5. The seven full-length TTV genomes were between 73.8% and 96.5 % identical to one another (Table 11).

Table 11. Pair wise comparison of amino acid sequences of ORF1, ORF2t, and ORF3 and the nucleotide sequences of the full and near full length genomes.

	SUZ11	AB008394*	AF079173*	A1-16	SUZ36	WD77	HTLV11	HTLV21	TTVsA4	HTLV12	Suz12
						Genome per cent identity					
SUZ11-ORF1		97.7	95.7	92.6	84.1	73.9	73.9	73.8	74.0	73.1	72.5
ORF2t											
ORF3											
AB008394*-ORF1	93.4		96.5	93.0	84.3	73.4	73.4	73.4	73.4	73.4	72.7
ORF2t	96.7										
ORf3	100.0										
AF079173*-ORF1	92.9	94.0		92.1	84.3	73.1	72.7	72.8	73.0	72.8	72.2
ORF2t	96.7	96.0									
ORF3	100.0	100.0									
A1-16-ORF1	92.9	94.0	93.5		85.6	74.1	74.0	74.1	74.4	73.6	73.3

ORF2t	96.0	96.0	94.7									
ORF3	94.8	94.8	94.8									
SUZ36-ORF1	86.2	87.4	86.1	89.1		74.2	74.0		74.2	74.1	74.1	73.0
ORF2t	77.5	76.8	75.5	78.1								
ORF3	79.3	79.3	79.3	81.0								
WD77-ORF1	67.2	68.4	66.8	66.5	68.6		95.7		96.5	92.6	73.5	73.2
ORF2t	51.0	51.7	49.7	53.0	52.3							
ORF3	74.1	74.1	74.1	75.9	74.1							
HTLV11-ORF1	66.3	67.7	65.9	65.6	67.8	94.3			95.7	91.7	73.3	72.9
ORF2t	51.0	51.7	49.7	53.7	51.7	94.0						
ORF3	79.3	79.3	79.3	79.3	74.1	89.7						
HTLV21-ORF1	66.7	68.1	66.1	65.9	67.8	95.4	93.5			92.4	73.8	73.2
ORF2t	51.0	51.7	49.7	53.7	53.0	97.3	94.7					
ORF3	70.7	70.7	70.7	70.7	72.4	93.1	86.2					
TTVsA4-ORF1	66.8	68.5	67.9	65.1	68.9	91.5	90.2		91.7		73.7	73.2
ORF2t	47.7	48.3	47.0	50.3	51.0	90.1	88.7		90.0			
ORF3	72.4	72.4	72.4	74.1	72.4	98.3	87.9		91.4			
HTLV12-ORF1	67.2	67.6	66.4	67.0	68.4	66.2	66.2		66.4	67.0		95.3
ORF2t	49.3	50.7	49.3	52.0	52.0	53.0	52.5		53.0	50.3		
ORF3	82.8	82.8	82.8	84.5	81.0	77.6	74.1		75.9	75.9		
Suz12-ORF1	67.1	67.2	66.2	66.6	68.1	67.3	66.6		67.8	67.4	93.7	
ORF2t	48.0	49.3	48.0	50.7	51.3	52.3	51.7		51.7	49.7	96.7	

ORF3	81.0	81.0	81.0	82.8	79.3	79.3	72.4	77.6	77.6	94.8		
							Amino acid per cent identity					

The partial genomes were 72.2% to 97.7% identical across the regions of overlap. Detailed regional comparisons performed by aligning the seven full length genomes and then plotting the percent identity within a sliding window of comparison, demonstrated approximately 80% identity across the entire length (Figure 5). Within these genomes, multiple regions of very high similarity (>90%), as well as several regions of extreme variability (<70%), were present. Inclusion of the four partial sequences did not dramatically alter these results.

Phylogenetic analysis was performed to determine the genetic relationship of the 7 full length and 4 near-full length genome sequences. Sequences were aligned and analysis performed across the region of overlap. Genetic distances suggested the presence of four distinct groups. Isolates TA278 (GenBank accession No. AB008394), TTVCHN1 (GenBank accession No. AF079173), GH1 (SEQ ID NO. 29), and JA9 (SEQ ID NO. 52) grouped closely to one another with distances of 0.0239 to 0.0805 substitutions per position. Isolates JA1 (SEQ ID NO. 54), JA4 (SEQ ID NO. 55), US32 (SEQ ID NO. 56) and US35 (SEQ ID NO. 57) grouped together with distances of 0.0352 to 0.0950 substitutions per position, however, these sequences segregate from the previous group with distances greater than 0.3879. Isolates JA2b (SEQ ID NO. 58) and JA10 (SEQ ID NO. 59) grouped independently from the above sequences with distances greater than 0.3919 substitutions. These two isolates had a pairwise distance of 0.0491. The final isolate, JA20, formed a

unique group with genetic distances between 0.1635 and 0.3941 to all other isolates.

An unrooted phylogenetic tree clearly demonstrated the relationship of these sequences to one another, forming four clusters, all supported by bootstrap values greater than 89% (Figure 6). The first of these (TA278, GenBank accession No. AB008394; TTVCHN1, GenBank accession No. AF079173; GH1, SEQ ID NO. 29; and JA9, SEQ ID NO. 52) represented isolates which have previously been characterized as genotype 1. Comparison with reported partial TT virus sequences suggested that these may be members of subtype 1a. The second cluster (JA1, SEQ ID NO. 54; JA4, SEQ ID NO. 55; US32, SEQ ID NO. 56; and US35, SEQ ID NO. 57) represented sequences of genotype 2, most similar to subtype 2b. The sequences of isolates JA2b (SEQ ID NO. 58) and JA10 (SEQ ID NO. 59) represented genotype 3 as defined in Example 5. The final isolate, JA20 (SEQ ID NO. 53), was most closely related to the genotype 1 sequences, yet grouped independently of these sequences. Comparisons to partial sequences demonstrated that this isolate represented subtype 1b. The presence of the 4 near full-length genomes did not alter these results, as the observed groupings were identical in their absence.

Example 6.3. Analysis of Open Reading Frames.

The availability of multiple diverse isolates also allowed the identification of conserved ORFs. Barring the isolation of viral proteins, the presence of a highly conserved ORF lends support to the possibility of an actual viral protein being synthesized from an ORF. The large open reading frame (Seq ID NO. 29, residues 589-2898, encoding a 770

amino acid protein, see Example 3) was conserved in all but one of 19 isolates, ranging from 765 to 770 amino acids in length (Table 8). The US32 ORF1 was interrupted by an in-frame stop codon. While it is possible that this was an artifact, analysis of multiple clones revealed identical sequence. A methionine was present immediately following the stop codon. Thus, it is possible that this isolate might produce two distinct proteins. Further experiments are necessary to address this issue. Among the full-length isolates, the amino acid sequences of ORF1 exhibited 65.1% to 95.6% identity (TABLE 11). The conserved initiating methionine codon (position 589 of GH1, SEQ ID NO. 29) resided within a Kozak motif for the efficient initiation of eucaryotic protein synthesis (Kozak, J. of Cell. Biol. 108:229-241 (1989)). Additionally, there was a conserved eucaryotic polyadenylation signal (AATAAA) located 177 nucleotides downstream from the ORF1 termination codon (position 2899 of GH1, SEQ ID NO. 29). This was the only polyadenylation signal conserved in all TT sequences.

The second ORF (nts 107-712 of SEQ ID NO. 29, encoding a 202 amino acids protein) was not conserved in all of the eleven TTV isolates examined. Though ORF2 was present in all genotype 1 sequences, nucleotide deletions were present in all genotype 2 and 3 sequences that resulted in a frameshift. A smaller version of ORF2 (SEQ ID NO. 29, nts 263-712, encoding a 149 to 151 amino acid protein) was conserved in all of the eleven isolates. Comparisons of this truncated ORF, ORF2t, demonstrated extreme sequence divergence, with as little as 47.0% amino acid sequence identity (Table 11). Contrary to ORF1,

the conserved methionine codon did not lie within an optimal Kozak sequence (Kozak, J. of Cell. Biol. 108:229-241 (1989)). However, residues incompatible with eucaryotic translation initiation at this site were not found.

A third open reading frame of 57 amino acids (nucleotides 2904-3074, SEQ ID NO. 29) was found in all eleven isolates. This ORF, ORF3, was located immediately downstream of ORF1, terminating at the conserved polyadenylation signal. Amino acid sequence comparisons demonstrated that ORF3 was greater than 70.7% conserved, the least variable of the three conserved ORFs (Table 11). There appeared to be no other ORFs longer than 30 nucleotides conserved in any of the six reading frames of all eleven full length and near full length sequences.

Example 6.4 Primer Design. As TT virus isolates have continued to be identified, researchers have attempted to design new PCR primers in an effort to improve PCR assay sensitivity. The majority of these utilize primers located within ORF1. Even though these primers have been successful at identifying multiple genotypes and subtypes of TT virus, the high degree of variability within the primer regions of ORF1 (greater than 10% divergence) may result in a large number of undetected positive samples. In fact, using first or second generation PCRs it is necessary to perform several distinct assays to estimate the prevalence of TT virus ((Simmonds et al., The Lancet 352:191-194 (1998)) and Example 4). Recently, a PCR assay employing primers designed within the first 200 nucleotides of the genome has demonstrated that 92% of healthy Japanese individuals are TT virus positive (Takahashi et al., Hepatol. Res. 12:233-239 (1998)).

While these primers exhibited much greater sensitivity compared to previous sets, they are designed solely to genotype 1 isolates and will not amplify genotype 2 specific sequences (data not shown). As genotype 2 and 3 isolates are also prevalent in Japan, it is possible that additional TT virus positive individuals would be identified with consensus primers designed from alignments of sequences representing all three genotypes. Utilizing full length and partial genome alignments from this study (Figure 5), three sets of consensus oligonucleotide primers have been designed which are able to detect genotype 1, 2, and 3 sequences. These primers and their use are described in Example 7.

Example 7. Third-generation TTV PCR primers

TT virus prevalence determined using first and second generation primers are thought to underestimate the true prevalence of TT virus in the populations examined to date (see Example 4). Recently, oligonucleotide primers have been described by Takahashi et al. (Takahashi et al., Hepatol. Res. 12:233-239 (1998)) that are 10-100 times more sensitive than those described by Okamoto et al. (Okamoto et al., Hepatol. Res. 10:1-16 (1998)) and Simmonds et al. (Simmonds et al., The Lancet 352:191-194 (1998)). Although these primers will only detect genotype 1 sequences (Leary and Erker, unpublished observations), 92% of healthy individuals in Japan were positive by this assay. Here, we present three nested PCR assays capable of detecting the most divergent isolates of TT virus known. These third-generation assays have superior sensitivity to all PCR assays previously described. Additionally, we have used these assays to demonstrate that TT virus is

present in the serum of a variety of distinct animal species, eliminating TT virus as an exclusively human virus and questioning its role as a causal agent in human liver disease.

Primer Design. Nucleotide sequence alignments were performed using the genome length sequences (SEQ ID NOS. 29, 52-57) from Example 6 to identify regions of conservation among the distinct isolates. Nested pairs of oligonucleotide primers were designed to three regions of the virus genome and examined for identity against partial TT virus sequences present in existing databases. Selected primers were tested by PCR for utility and sensitivity utilizing several previously identified serum samples known to be of high titer. Three sets of PCR primers were PCR primers were subjected to extensive testing: Set A forward 1 (SEQ ID NO. 60); Set A reverse 1 (SEQ ID NO. 61); Set A forward 2 (SEQ ID NO. 62); Set A reverse 2 (SEQ ID NO. 63); Set B forward 1 (SEQ ID NO. 64); Set B reverse 1 (SEQ ID NO. 65); Set B forward 2 (SEQ ID NO. 66); Set B reverse 2 (SEQ ID NO. 67); Set C forward 1 (SEQ ID NO. 68); Set C reverse 1 (SEQ ID NO. 69); Set C forward 2 (SEQ ID NO. 70); Set C reverse 2 (SEQ ID NO. 71).

PCR Assays. Total nucleic acids were extracted from 25 or 50 μl of serum using the RNA/DNA Isolation Kit (Amersham Life Science Inc., Arlington Heights, IL) as directed by the manufacturer. Dried nucleic acid pellets were then dissolved in 25 or 50 μl of water corresponding to the initial serum volume. First round PCR reactions (10 μl volume) utilized 1.0 μM final concentration of each primer, 2 μl of total nucleic acids and the GeneAmp PCR Reagent Kit (Perkin Elmer, Foster City, CA) as specified by the

manufacturer with a final $MgCl_2$ concentration of 2.0 mM. Nested PCR reactions (25 μl) utilized 0.5 μM final concentration of each primer, 1 μl of the first round PCR product as template and the conditions described above. Amplification was for 35 cycles (20 seconds at 94°; 30 seconds at 55°C; 30 seconds at 72°C) followed by a 10 minute extension at 72°C. Nested PCR products were separated by electrophoresis through a 1.2% agarose gel, blotted onto a nylon membrane and analyzed by Southern hybridization to score positive results.

Phylogenetic Analysis. Nested PCR products were gel isolated, then excised and purified with Geneclean II (Bio101, Vista, CA). Purified products were ligated into pGEM-T Easy (Promega, Madison, WI) and each strand was sequenced with ABI Big Dye and analyzed on the Applied Biosystems model 377 DNA sequencer. Sequences were edited and assembled utilizing Sequencher version 3.0 (Gene Codes Corp., Ann Arbor, MI) and analyzed using the programs of the Wisconsin Sequence Analysis Package (Version 9.0, Genetics Computer Group, Madison, WI). Sequence alignments were performed utilizing the GAP program with the default settings in place for gap creation and extension. Phylogenetic distances between pairs of nucleotides were determined using DNADIST, and the distances between pairs of the amino acids were determined by the PRODIST program (Felsenstein, (1993)) of the PHYLIP package (version 3.5c). These computed distances were utilized for the construction of phylogenetic trees using the programs NEIGHBOR and RETREE. The final output was generated with the use of TREEVIEW (Page, Computer Applications in the Biosciences 12:357 (1996)). Bootstrap values were

determined on 100 resamplings of the nucleotide or amino acids sequences, respectively, using SEQBOOT, DNADIST or PROTDIST, NEIGHBOR and CONSENSE. Values greater than 70% were considered supportive of the observed groupings.

Performance of the third generation PCR assays.

The present inventors compared the primer sets against previously reported PCR assays for the detection of TT virus by testing a serum panel of 48 normal donors of which approximately 25% had been previous shown to be TT virus positive by first- and second-generation TTV PCR assays. As shown in Table 12, 38 (79.2%) of the samples were found to be positive by at least one of the third-generation assays and 24 (50.0%) were positive by 2 or more assays.

Table 12

Sample	Nishizawa	Okamoto	Simmonds	Set A	Set B	Set C
1						+
2		+			+	
3				+	+	
4		+	+			
5	+				+	
6			+			
7					+	+
8		+				+
9					+	+
10				+	+	+
11						+
12						
13					+	+
14					+	
15						+
16						
17						+
18						
19		+	+	+	+	+

20		+	+	+	+	+
21						
22					+	
23						
24				+	+	
25				+	+	+
26					+	
27						+
28				+	+	+
29	+			+	+	+
30						
31						
32						
33					+	
34			+		+	
35			+		+	+
36		+	+	+	+	+
37						
38					+	
39				+	+	
40						
41	+				+	+
42					+	
43						+
44				+	+	+
45			+	+	+	+
46		+			+	+
47		+	+	+	+	+
48					+	
Total	3	8	9	13	29	23

Set A detected 13 (27.1%) samples, Set B, 29 (60.4%) samples, and Set C, 23 (47.9%) samples. Previously described PCR assays for TT virus by Nishizawa, Okamoto and Simmonds detected 3 (6.3%), 8 (16.7%), and 9 (18.8%) samples, respectively. Though none of the samples are positive in all assays, Set B and Set C assays are clearly superior to any of the others. Set

B detected 76.3% of the positive samples while Set C detected 60.5%. In combination, Set B and Set C detect 36 of the 38 (94.7%) of the positive samples though only 42.1% are detected by both assays. These results are not surprising as TT virus has been previously shown to have significant divergence at the nucleic acid level, finding which can have dramatic effects on molecular based assays. In addition, it is possible to use different combinations of the primers described above. Specifically, we have used the forward primers from set A and the reverse primers form set B in nested PCR (SEQ ID NO:64 and SEQ ID NO:69, followed by SEQ ID NO:66 and SEQ ID NO:71) to detect 14 of 38 (36.8%) of the TTV-positive samples detected in table 12 (data not shown).

Because the new primer pairs described above appear to be superior to those previously reported, a number of populations previously evaluated for the presence of TT virus (Example 4) were reexamined utilizing Set B primers (Table 13).

Table 13

Population	Set B Positive	Percent Positive	Previously Positive*
Volunteer Blood Donors (n= 91)	31	34.1	10.7
Volunteer Blood Donors (High ALT n=69)	11	15.9	9.1
Commercial Blood Donors (n=48)	19	39.6	12.8
Injectable Drug Users (n=82)	67	81.7	17.2
Hemophiliacs (n=73)	70	95.9	56.2
New Zealand Children (n=36)	8	22.2	11.1
Non A-E Hepatitis Cases (n=47)	28	59.6	2.1
Japanese Individuals (n=20)	20	100.0	35.0

* See Example 5

Among volunteer blood donors with normal ALT levels, 31 (34.1%) were found to be positive for TT virus.

This is as compared to 10.7% previously found to be positive with two distinct primer pairs. When volunteer blood donors with elevated ALT values were examined, 11 (15.9%) were positive as compared to the 9.1% determined previously for this population. Commercial blood donors that were 12.8% positive by the two primer pairs are currently 39.6% positive utilizing Set B primers. Further, injectable drug users that were 17.2% positive in the previous study were 81.7% positive with Set B primers. Finally, among 48 non A-E hepatitis samples tested, only 1 was positive utilizing the two primer pairs while 59.6% were positive in the existing assay.

Additionally, the present inventors have tested a number of other populations and have compared the results to the previous standard of the sum of two distinct primer pairs (data not shown). Hemophiliacs, which were 56.2% positive by the combination of two previous assays, were 95.9% positive with the Set B primer assay. Japanese blood donors that were previously 35.0% positive were now 100% positive, and the rate was double (22.2% as compared to 11.1%) in a panel of New Zealand children utilizing the Set B primer assay. Most remarkable in these comparisons is that virtually all samples previously determined to be TT virus positive were detected with the Set B primer assay. This was not the case in the limited study initially conducted with these primers (Table 12). Also examined were limited samples from several species of non-human primates. TT virus was detected in tamarins (23.5%), owl monkeys (20.0%) and chimpanzees (50.0%), while virus sequences were not detected in calithrix, mystax or macaques. Caution must be used in evaluating these data for a number of

reasons: 1.) the number of samples tested from each species was very limited; 2.) the possibility that the animals being tested were at one time inoculated with human materials can not be eliminated, and; 3.) it is conceivable that these samples were infected with a related virus that is being detected as a result of a highly conserved region present in the two viruses. Though the products amplified from these animals are very similar by sequence analysis to the human isolates detected, it is not possible eliminate this final point as these sequences have not been extended beyond the amplified region.

As a result of the high viral prevalence, the present inventors were interested in determining the source of human infection. Because the rate of infection between volunteer blood donors and patients with non A-E hepatitis was not substantially different, it was surmised that the source would be common regardless of geographic location. Therefore, it was decided to test for the presence of TT virus in the serum of domesticated food animals utilizing the Set B primer assay. As demonstrated in Table 14, 20% of pigs, 25% of cows, 30% of sheep and 19% of chickens were positive for the presence of TT virus. Sequence determination and

Table 14. The presence of TTV in farm animals.

Group	Set B Positive	Percent Positive
Porcine (n=20)	4	20.0%
Bovine (n=20)	5	25.0%
Ovine (n=20)	6	30.0%
Chicken (n=21)	4	19.0%

phylogenetic analyses demonstrate that these sequences are similar to others detected with Set B primers, though the sequences do not cluster independently from the human isolates within this region (Figure 7). In fact, the animal isolates are much more closely related to the human sequences than the human sequences are to one another. Of significance is the fact that only three of these animals are positive when tested with three previously described PCR assays (Nishizawa et al., Biochem Biophys Res Commun 241:92-97 (1997; Okamoto et al., Hepatol. Res. 10:1-16 (1998; Simmonds et al., The Lancet 352:191-194 (1998)).

Example 8. Use of TTV Sequence Diversity to Track Transmission of the Virus.

An actual application of this method is presented in Example 1. The infectious nature of human TTV and the parenteral transmissibility of the virus to chimpanzees was demonstrated by the complete conservation of TTV sequences between source and recipient indicating that TTV infection was derived from its corresponding inoculum. In the following prophetic example, transmission of TTV between individuals is monitored by comparison of TTV DNA sequences obtained from the individuals involved.

Serum total nucleic acids (25 µl) are extracted from 2 or more individuals of interest using the DNA/RNA Extraction kit (Amersham Life Science Inc., Arlington Heights, IL). Nucleic acids are dissolved in 25 µl of nuclease-free water and 4 µl are used as template in the amplification reactions. Oligonucleotide primers can be, but are not limited to, those described by Nishizawa (Nishizawa et al., Biochem Biophys Res Commun 241:92-97 (1997)) (SEQ ID

NOS. 32 and 33 followed by SEQ ID NOS. 34 and 35) or Simmonds (Simmonds et al., The Lancet 352:191-194 (1998)) (SEQ ID NOS. 1 and 2 followed by SEQ ID NOS.3 and 4) or those described in example 7 (SEQ ID NOS. 60 and 61 followed by SEQ ID NOS. 62 and 63, or SEQ ID NOS. 64 and 65 followed by SEQ ID NOS. 66 and 67, or SEQ ID NOS. 68 and 69 followed by SEQ ID NOS. 70 and 71). Amplification reactions (20 µl) are performed for thirty-five cycles (94°C for 20 seconds, 55°C for 30 seconds, and 72°C for 30 seconds) and contain 1.0 µM final concentration each primer and 1.5 units of Taq DNA polymerase (Perkin-Elmer, Foster City, CA). Nested PCR reactions are performed on 1.0 µl of the primary PCR reaction using the same amplification conditions as above. PCR products are purified by 2% agarose gel electrophoresis with visualization via ethidium bromide fluorescence, and are subsequently purified by excision and extraction of DNA. The amplification products encompass a region of known high variability and are sufficiently large such that the chance of two isolates having the exact, or nearly exact, nucleic acid sequence is minimized. Amplification products are sequenced, either partially or in full, and sequences are aligned using the program PILEUP (Wisconsin Package, version 9.0). PCR primer sequences are not included in the sequence alignment which is utilized to determine the percent identity between isolates. The more similar the TTV sequences are to one another, the more likely it is that the individuals involved were infected from a common source or that one individual infected the other.

This example also has applications to fields such as forensics. In this embodiment, comparison of TTV genomic sequences is used to establish previous contact between individuals and, depending on the mode of transmission, what the nature of the contact might be.

Example 9. Use of TTV as a Vector

In this example, construction of a TTV-based vector is described, along with its use in expressing foreign nucleic acids and/or proteins in eucaryotic cells. Other means of construction and applications of the TTV vector will be apparent to those of ordinary skill of the art when considering this disclosure.

An entire TTV genome is cloned in double stranded form, either as a single piece or in multiple fragments, as described in example 3 for isolate GH1 using anchored PCR. If obtained as multiple clones, the TTV genome is re-assembled into a single clone containing a plasmid-based replicon capable of propagation and selection in bacteria. The positions within the TTV genome sequence of the plasmid replicon and of a polylinker region containing multiple cloning sites are determined by the biology of TTV. For example, the sites should not interfere with desired properties of the vector, such as the ability to infect cells, replication, virion formation and propagation of infection. Other sequences are also required for vector function, and are derived either from TTV or other sources. These can include transcriptional controls (e.g. promoter, stop, polyadenylation and enhancer sequences) and expressions controls (e.g. Kozak sequences). The

capacity of TTV to carry these additional sequences and remain functional, is evaluated by transfection of experimental vector constructs into a permissive eucaryotic cell line. Similarly, TTV sequences, non-essential to vector function, can be eliminated in order to increase the amount of foreign DNA the vector can accommodate.

A DNA fragment of interest (e.g. containing a protein binding site or encoding a RNA or protein) is inserted into the TTV vector cloning site and the ligated product is amplified in bacteria and then introduced into cell culture. The effect that the cloned insert has on the cells is studied, or the expressed product (e.g. any protein of interest such as an enzyme, antigen or recombinant vaccine protein) is isolated.

Alternatively, gene therapy of a host such a domesticated animal (e.g. cat, dog, pig, chicken, sheep or cow), primate or human can be performed using virions isolated from cell culture and used to infect the host. Infection of the host may also be possible by direct injection of the purified DNA vector into the animal. The infected host is monitored for effects of the vector insert (e.g. appearance of antibodies to an expressed vaccine antigen, compensation for a genetic defect by expression of a corrective gene, suppression of a harmful host gene by production of antisense RNA, production of medically or commercially useful products).

In other embodiments of this example:

(a) Portions of the TTV genome such as origin of replication, transcriptional controls, genes, packaging signals etc., are used as components of other eucaryotic vectors.

(b) A TTV-based episomal vector is constructed which contains deletions making it unable to infectious virions, and therefore not transmissible.

(c) A TTV-based helper virus system is constructed in which one or both members are derived from TTV, and in which one vector provides function(s) necessary for the production of virions from the other vector.

(d) A family of closely related TTV vectors is constructed as described above. Members of the family vary in those regions of the TTV genome that encode epitopes recognized by the immune system of a host, resulting in clearance of the vector. The epitope-encoding region for each vector is derived from a TTV isolate that does not show shared immunity with any of the other members of the vector family. Existence of such non-cross reactive TTV isolates is strongly suggested by the demonstration of co-infections and the high prevalence level in humans. An individual who has developed immunity to the initial vector, is treated with another member of the vector family to which immunity has not developed. Sequential treatment with different members of the vector panel described above is used to maintain or repeat therapy, a common problem with DNA virus-based gene therapy.

The primers of the present invention described herein thus are useful for detecting TTV in individuals. Other uses or variations of the present invention will be apparent to those of ordinary skill of the art when considering this disclosure.

CAGACAGAGGAGAAGGCAACATG A5430
;
TACCAYTTAGCTCTCATTCTWA A5427m
;
GGMAAYATGYTRTGGATAGACTGG A8761
;
CTACCTCCTGGCATTTTACCA A5432
;
GATGGTGCAAACYTTTGCCTCC B19-FORWARD
;
GCATGACTTCAGTTAATTCTGCA B19-REVERSE
;
AGACAGAGGAGAAGGCAACA TTVjs-s1
;
GACCAAAACATACACATGAA TTVjs-a1
;
GTAAGCGGGAACACTACAAC B19.1699-s1
;
CGGAGGAAACTGGGCTTCCG B19.2119-a1
;
CTAGCTGCACTTCCGAATGGCTG TTV-JIM1?
;
GGTACTGTTGGTCATTGCGAGGTGG TTV-JIM2?
;
GTGAAGCCACGGAGGGAGATCAG TTV-jim3?
;
CCTGGCATCTTTCCATTTCCAAAG A1
;
GACTGGCTAACTAAAGATACCTCAG S2
;
TCCAAAGTTAAAACTGTAGGGTACG A2
;
GGGTCTGTGTGTACTAAGAGTTGG N22-A1
;
AAAGTCTGGCATTCATGTGTATG N22-A2
;
GCCAGGAGGTAGCAGCAATGTGC N22-S1
;
CTATTAGAATGAGAGCTAAGTGGTACC N22-S2
;
GCTAAGTACACTTGAGTACCATTGC UFGH1-A1
;
GGTACTGTTGGTCATTGCGAGGTGG UFGH1-A2
;
CTGGAAGGAAGAGTATGAGGCCTG DFGH1-S1
;
CCCTAGAGGCAATCTAAGAGACACC DFGH1-S2
;
AGCCTTTTGTGGGGTCTGTGTGTACTA UFTTV1
;
TGGAAATGGTAAAATGCCAGGAGGTAG DFTTV1

;
GTCTGGCATTCATGTGTATGTTTTGGTC UFTTV2
;
GCAGCAATGTGCCTATTAGAATGAGAGC DFTTV2
;
TTTGTGCTACGTCACTAACCACGTGACGCCCACAGGCCAACCGAATGCTATGTC
GTGCACTTCCTGGGCCGGGTCTACGTCCTGATATAACTAGCTGCACTTCCGAAT
GGCTGAGTTTTCCACGCCCGTCCGCAGCGGTGAAGCCACGGAGGGAGATCAGCG
CGTCCCGAGGGCGGGTGCCGGAGGTGAGTTTACACACCGGAGTCAAGGGGCAAT
TCGGGCTCGGGACTGGCCGGGCTATGGGCAAGGCTCTGAAAAAAGCATGTTTAT
CGGCAGGCATTACAGAAAGAAAAGGGCGCTGTCACTGCTTGCTGTGCGAACAAC
ACAGAAGGCTCGCAAACTACTAATAGTGATGTGGACCCCACCTCGCAATGACCA
ACAGTACCTCAACTGGCAATGGTACTCAAGTGTACTTAGCTCCCACGCTGCTAT
GTGCGGGTGTCCCGACGCTGTCGCTCATTTTAATCATCTTGCTTCTGTGCTTCG
CGCCCCGCAAAATCCACCCCCGCCCGGTCCCCAGCGAAACCTGCCCCTCCGACG
GCTGCCAGCTCTCCCGGCTGCGCCAGAGGCGCCCGGAGATAGAGCACCATGGCC
TATGGCTGGTGGCGCCGAAGGAGAAGAAGGTGGCGCAGGTGGCGACGCAGACCA
TGGAGGCGCCGCTGGAGGACCCGAAGACGCAGACCTGCTAGACGCCGTGGCCGC
CGCAGAAACGTAAGGAGACGGCGCCGAGGAGGGAGGTGGAGGAGGAGGTACAGG
AGATGGAAAAGAAAGGGCAGGCGGAGAAAGAAAGCTAAAATAATAATAAGACAA
TGGCAACCAAACTACAGGAGGAGATGTAACATAGTGGGCTACATTCCCGTACTG
ATATGTGGCGAAAATACTGTCAGCAGAAACTATGCCACACACTCAGACGATACC
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;
GCTGCACTTCCGAATGGCTGAG SetAforward1
;
CCACCAGCCATAGGCCATGGTG SetAreverse1

;
GAGTTTTCCACGCCCGTCCGC SetAforward2
;
CCAGCCATAGGCCATGGTGCTC SetAreverse2
;
GTGGGACTTTCACTTGTCGGTGTC SetBforward1
;
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;
AGGTCACTAAGCACTCCGAGCG SetBforward2
;
GCGAAGTCTGGCCCCACTCAC SetBreverse2
;
CAGACTCCGAGTTGCCATTGGAC SetCforward1
;
CACGTGTCGGGGCCTACTTCCG SetCreverse1
;
GCAACGAAAGTGAGTGGGGCCAG SetCforward2
;
GGTTTCCGCCGAGGATGACCT SetCreverse2

We Claim:

1. A probe or primer specific for TT virus selected from the group consisting of SEQ ID NO:29, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70 and SEQ ID NO:71.

2. The probe or primer of claim 1, wherein said probe or primer is selected from the group consisting of SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62 and SEQ ID NO:63.

3. The probe or primer of claim 1, wherein said probe or primer is selected from the group consisting of SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, and SEQ ID NO:67.

4. The probe or primer of claim 1, wherein said probe or primer is selected from the group consisting of SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, and SEQ ID NO:71.

5. A method for detecting the presence of TTV target nucleotides which may be present in a test sample comprising the steps of:

(a) contacting a test sample suspected of containing a target TTV nucleotide sequence with a TTV primer pair consisting of: 1) SEQ ID NO:60 and 2) a primer selected from the group consisting of SEQ ID

NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71, to form a reaction mixture which generates a product;

(b) contacting said reaction mixture with a TTV primer pair consisting of: 1) SEQ ID NO:62 and 2) a primer selected from the group consisting of SEQ ID SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71, wherein the nucleotide sequence of said selected primer hybridizes with said product of said reaction mixture of (a); and

(c) detecting the presence of the TTV target nucleotide in said test sample.

6. The method of claim 5 wherein said primer pair of step (a) consists of SEQ ID NO:60 and SEQ ID NO:61, and said primer pair of step (b) consists of SEQ ID NO:62 and SEQ ID NO:63.

7. A method for detecting the presence of TTV target nucleotides which may be present in a test sample comprising the steps of:

(a) contacting a test sample suspected of containing a target TTV nucleotide sequence with a TTV primer pair consisting of: 1) SEQ ID NO:64 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71, to form a reaction mixture which generates a product;

(b) contacting said reaction mixture with a TTV primer pair consisting of: 1) SEQ ID NO:66 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ

ID NO:69 and SEQ ID NO:71, wherein the nucleotide sequence of said selected primer hybridizes with said product of said reaction mixture;

(c) detecting the presence of the TTV target nucleotide in said test sample.

8. The method of claim 7 wherein said primer pair of step (a) consists of SEQ ID NO:64 and SEQ ID NO:65, and said primer pair of step (b) consists of SEQ ID NO:66 and SEQ ID NO:67.

9. A method for detecting the presence of TTV target nucleotides which may be present in a test sample comprising the steps of:

(a) contacting a test sample suspected of containing a target TTV nucleotide sequence with a TTV primer pair consisting of: 1) SEQ ID NO:68 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO;67, SEQ ID NO:69 and SEQ ID NO:71, to form a reaction mixture which generates a product;

(b) contacting said reaction mixture with a TTV primer pair consisting of: 1) SEQ ID NO:70 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71, wherein the nucleotide sequence of said selected primer hybridizes with said product of said reaction mixture; and

(c) detecting the presence of said target TTV nucleotide in said test sample.

10. The method of claim 9 wherein said primer

pair of step (a) consists of SEQ ID NO:68 and SEQ ID NO:69, and said primer pair of step (b) consists of SEQ ID NO:70 and SEQ ID NO:71.

11. The method of claims 5, 7 or 9 wherein said test sample is isolated from a human or an animal.

12. A test kit for detecting target TTV nucleotides in a test sample, comprising:

(a) a container containing a primer pair specific for a TTV target nucleotide, wherein said primer pair consists of 1) SEQ ID NO:60 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71;

(b) a container containing a primer pair specific for TTV, wherein said primer pair consists of 1) SEQ ID NO:62 and 2) a primer selected from the group consisting of is SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO;69 and SEQ ID NO:71.

13. The test kit of claim 12 wherein said primer pair of (a) consists of SEQ ID NO:60 and SEQ ID NO:61, and said primer pair of (b) consists of SEQ ID NO:62 and SEQ ID NO:63.

14. A test kit for detecting target TTV nucleotides in a test sample, comprising:

(a) a container containing a primer pair specific for a TTV target nucleotide, wherein said primer pair consists of 1)SEQ ID NO:64 and 2) a primer selected from the group consisting of SEQ ID NO:61,

SEQ ID NO:63, SEQ ID NO:65. SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71;

(b) a container containing a primer pair specific for TTV, wherein said primer pair consists of 1) SEQ ID NO:66 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71.

15. The test kit of claim 14 wherein said primer pair of (a) consists of SEQ ID NO:64 and SEQ ID NO:65, and said primer pair of (b) consists of SEQ ID NO:66 and SEQ ID NO:67.

16. A test kit for detecting target TTV nucleotides in a test sample, comprising:

(a) a container containing a primer pair specific for a TTV target nucleotide, wherein said primer pair consists of: 1) SEQ ID NO:68 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71;

(b) a container containing a primer pair specific for TTV, wherein said primer pair consists of: 1) SEQ ID NO:70 and 2) a primer selected from the group consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69 and SEQ ID NO:71.

17. The test kit of claim 16 wherein said primer pair of (a) consists of SEQ ID NO:68 and SEQ ID NO:69, and said primer pair of (b) consists of SEQ ID NO:70 and SEQ ID NO:71.

18. The method of claims 12, 14, or 16 wherein said test sample is isolated from a human or an animal.

19. A TTV-based vector comprising: 1) a promoter; 2) a heterologous DNA sequence; and 3) a nucleotide sequence encoding TTV, a fragment of said nucleotide sequence or a complement of said nucleotide sequence or said fragment, wherein said heterologous DNA sequence is operably linked to said promoter.

20. The vector of claim 19 wherein said promoter is derived from TTV or from a heterologous source.

21. The vector of claim 20 wherein said heterologous DNA sequence comprises a polynucleotide sequence that is complementary to a targeted RNA sequence.

22. The vector of claim 20 wherein said heterologous DNA sequence encodes a protein.

23. The vector of claim 20 wherein said vector is capable of being packaged into TTV particles for stable maintenance or expression of said heterologous DNA sequence.

24. A host cell comprising said vector of claim 19.

25. The host cell of claim 24 wherein said cell is eukaryotic.

26. A method of expressing said heterologous DNA sequence of claim 19 or a product encoded by said heterologous DNA sequence, in a host, comprising introducing said vector of claim 19 into said host for a time and under conditions sufficient for expression of said heterologous DNA sequence or product encoded thereby.

27. A method of detecting transmission of TTV from one individual to another comprising the steps of:

(a) obtaining a biological sample from an individual having TTV;

(b) isolating a TTV DNA sequence from said biological sample;

(c) obtaining a biological sample from a second individual having TTV;

(d) isolating a TTV DNA sequence from said biological sample of said second individual;

(e) comparing said TTV DNA sequence of said first individual with said TTV DNA sequence of said second individual, identity between said DNA sequence of said first individual and said DNA sequence of said second individual indicating transmission of TTV from one individual to the other.

28. A method of determining TTV-infection in a tissue or organ prior to transplantation or xenotransplantation of said tissue or organ comprising the steps of:

(a) contacting a biological sample suspecting of

containing a TTV target nucleotide sequence, from a potential donor human or animal, with a TTV primer pair represented by SEQ ID NO:60 and SEQ ID NO:61 to form a first reaction mixture;

(b) contacting said reaction mixture with a TTV primer pair represented by SEQ ID NO:62 and SEQ ID NO:63 in order to form a second reaction mixture; and

(c) detecting the presence of the TTV target nucleotide in said test sample, presence of said nucleotide indicating TTV-infection in said biological sample and in said tissue or organ.

29. A method of determining TTV-infection in a tissue or organ prior to transplantation or xenotransplantation of said tissue or organ comprising the steps of:

(a) contacting a biological sample suspecting of containing a TTV target nucleotide sequence, from a potential donor human or animal, with a TTV primer pair represented by SEQ ID NO:64 and SEQ ID NO:65, to form a first reaction mixture;

(b) contacting said reaction mixture with a TTV primer pair represented by SEQ ID NO:66 and SEQ ID NO:67; and

(c) detecting the presence of the TTV target nucleotide in said test sample, presence of said nucleotide indicating TTV-infection in said biological sample and in said tissue or organ.

30. A method of determining TTV-infection in a tissue or organ prior to transplantation or

xenotransplantation of said tissue or organ comprising the steps of:

(a) contacting a biological sample suspecting of containing a TTV target nucleotide sequence, from a potential donor human or animal, with a TTV primer pair represented by SEQ ID NO:68 and SEQ ID NO:69, to form a first reaction mixture;

(b) contacting said reaction mixture with a TTV primer pair represented by SEQ ID NO:70 and SEQ ID NO:71; and

(c) detecting the presence of the TTV target nucleotide in said test sample, presence of said nucleotide indicating TTV-infection in said biological sample and in said tissue or organ.

31. The method of claims 28, 29, or 30 wherein said biological sample is selected from the group consisting of blood, tissue and an organ.

32. A method of detecting the presence of target TTV nucleotides in a test sample, comprising the steps of:

(a) contacting a test sample suspecting of containing a target TTV nucleotide with a primer pair represented by SEQ ID NO:60 and SEQ ID NO:61, to form a reaction mixture;

(b) contacting said reaction mixture with at least one TTV probe selected from the group consisting of SEQ ID NO:62 and SEQ ID NO:63; and

(c) detecting the presence of said target TTV nucleotide in said test sample.

33. The method of claim 32, wherein said at least one probe is conjugated to a detectable signal-generating compound.

34. The method of claim 33 wherein said detectable signal generating compound is selected from the group consisting of a chemiluminescent compound, fluorescein and an enzyme.

35. The method of claim 32 wherein said at least one probe is conjugated to an antibody.

36. A method of detecting the presence of target TTV nucleotides in a test sample, comprising the steps of:

(a) contacting a test sample suspecting of containing a target TTV nucleotide with a primer pair represented by SEQ ID NO:64 and SEQ ID NO:65 to form a reaction mixture;

(b) contacting said reaction mixture with at least one TTV probe selected from the group consisting of SEQ ID NO:66 and SEQ ID NO:67; and

(c) detecting the presence of said target TTV nucleotide in said test sample.

37. The method of claim 36, wherein said at least one probe is conjugated to a detectable signal-generating compound.

38. The method of claim 37 wherein said

detectable signal generating compound is selected from the group consisting of a chemiluminescent compound, fluorescein and an enzyme.

39. The method of claim 36 wherein said at least one probe is conjugated to an antibody.

40. A method of detecting the presence of target TTV nucleotides in a test sample, comprising the steps of:

(a) contacting a test sample suspecting of containing a target TTV nucleotide with a primer pair represented by SEQ ID NO:68 and SEQ ID NO:69 to form a reaction mixture;

(b) contacting said reaction mixture with at least one TTV probe selected from the group consisting of SEQ ID NO:70 and SEQ ID NO:71; and

(c) detecting the presence of said target TTV nucleotide in said test sample.

41. The method of claim 40, wherein said at least one probe is conjugated to a detectable signal-generating compound.

42. The method of claim 41, wherein said at least one probe is conjugated to a detectable signal-generating compound.

43. The method of claim 40, wherein said at least one probe is conjugated to a detectable signal-generating compound.

44. A method of detecting TTV target nucleotides which may be present in a test sample comprising:

(a) contacting said test sample suspected of containing a target TTV nucleotide sequence with a TTV primer pair consisting of 1) a primer selected from the group consisting of: SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, and SEQ ID NO:70, and 2) a primer selected from the group consisting: SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, and SEQ ID NO:71, to form a reaction mixture which generates a product;

(b) contacting said reaction mixture with a TTV primer pair consisting of: 1) a primer selected from the group consisting of: SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, and SEQ ID NO:70, wherein the nucleotide sequence of said selected primer hybridizes with said product of said reaction mixture and 2) a primer selected from the group consisting: SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, and SEQ ID NO:71, wherein the nucleotide sequence of said selected primer hybridizes with said product of said reaction mixture, and

(c) detecting the presence of the TTV target nucleotide in said test sample.

Figures

Figure 1

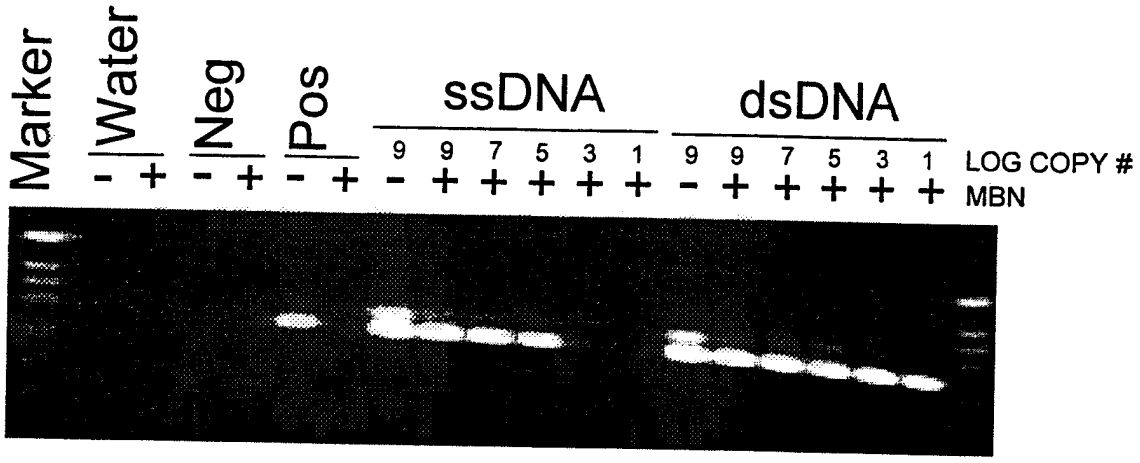
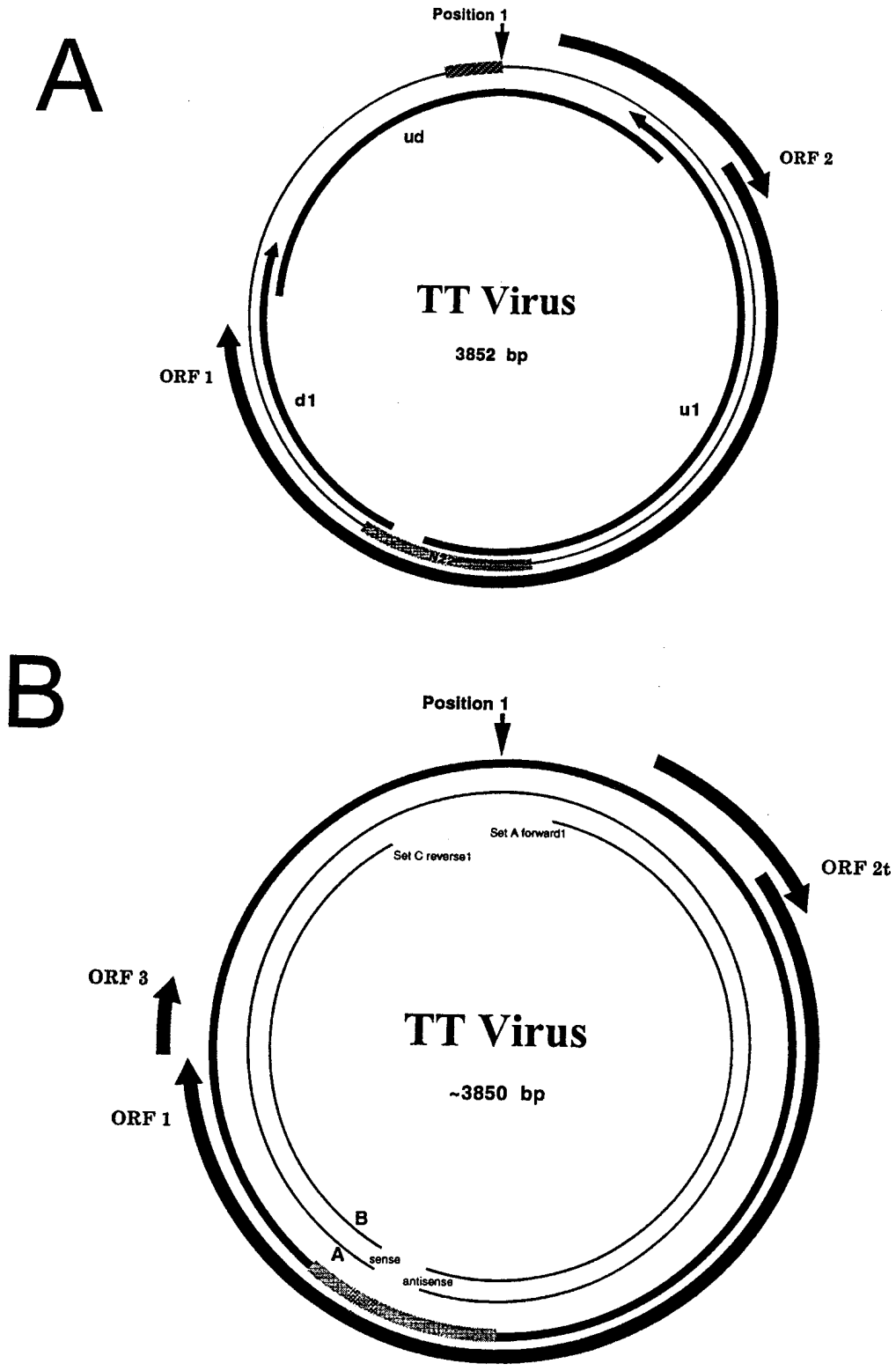


Figure 2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ORF 1
B
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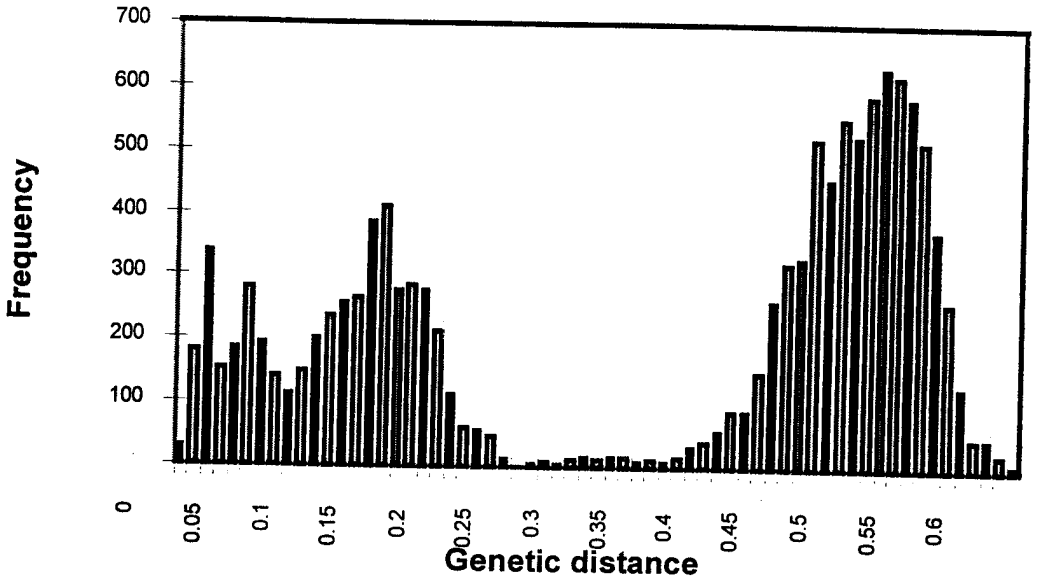
sense
antisense

Figure 3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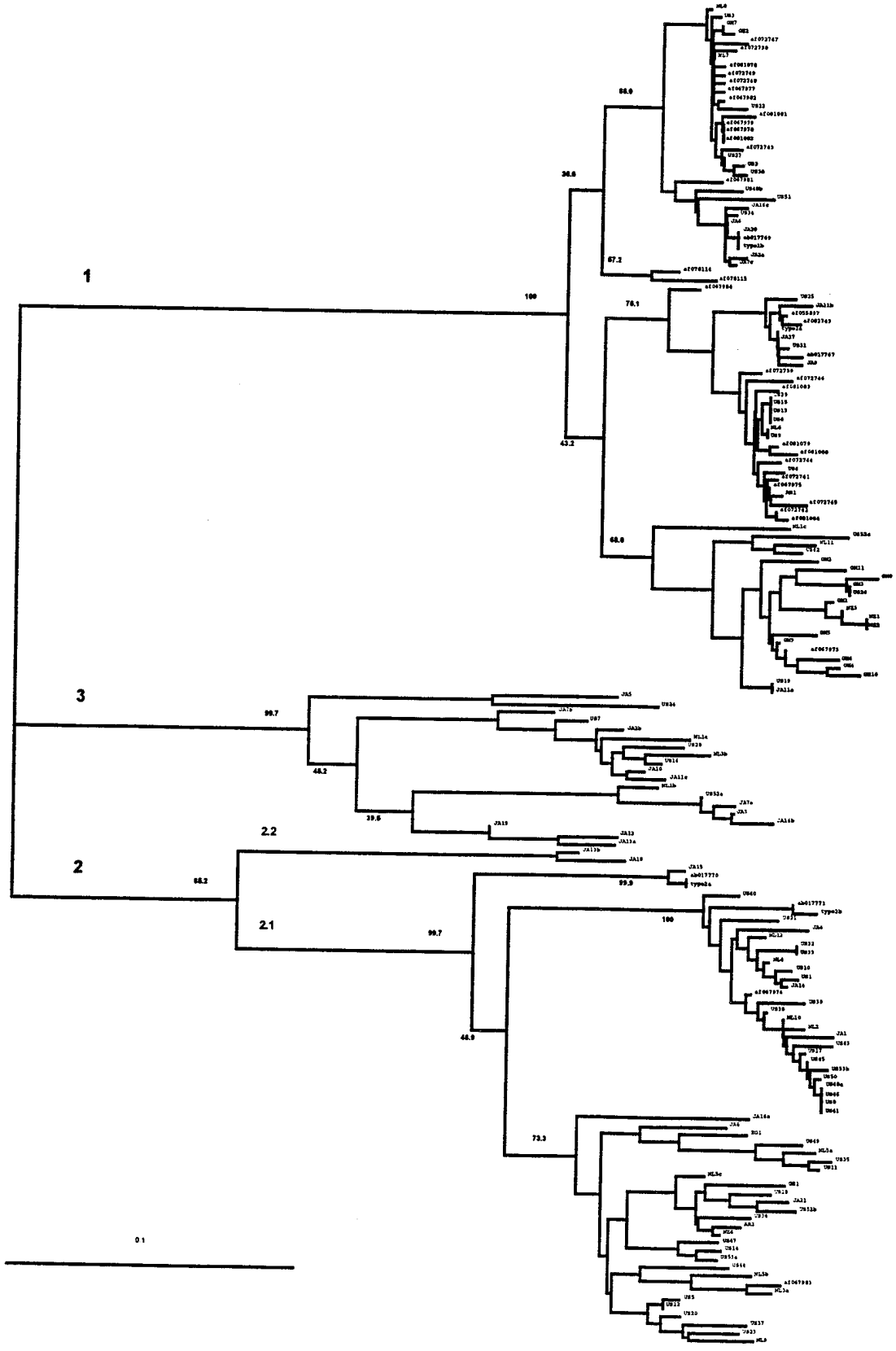
0.55
0.6
Genetic distance

Figure 4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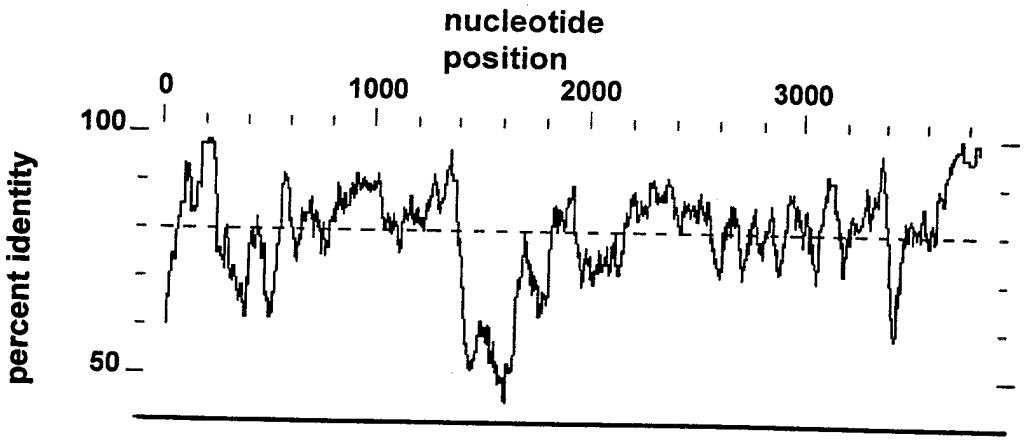
73.3
0.1

Figure 5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3000
100
50
percent identity

Figure 6

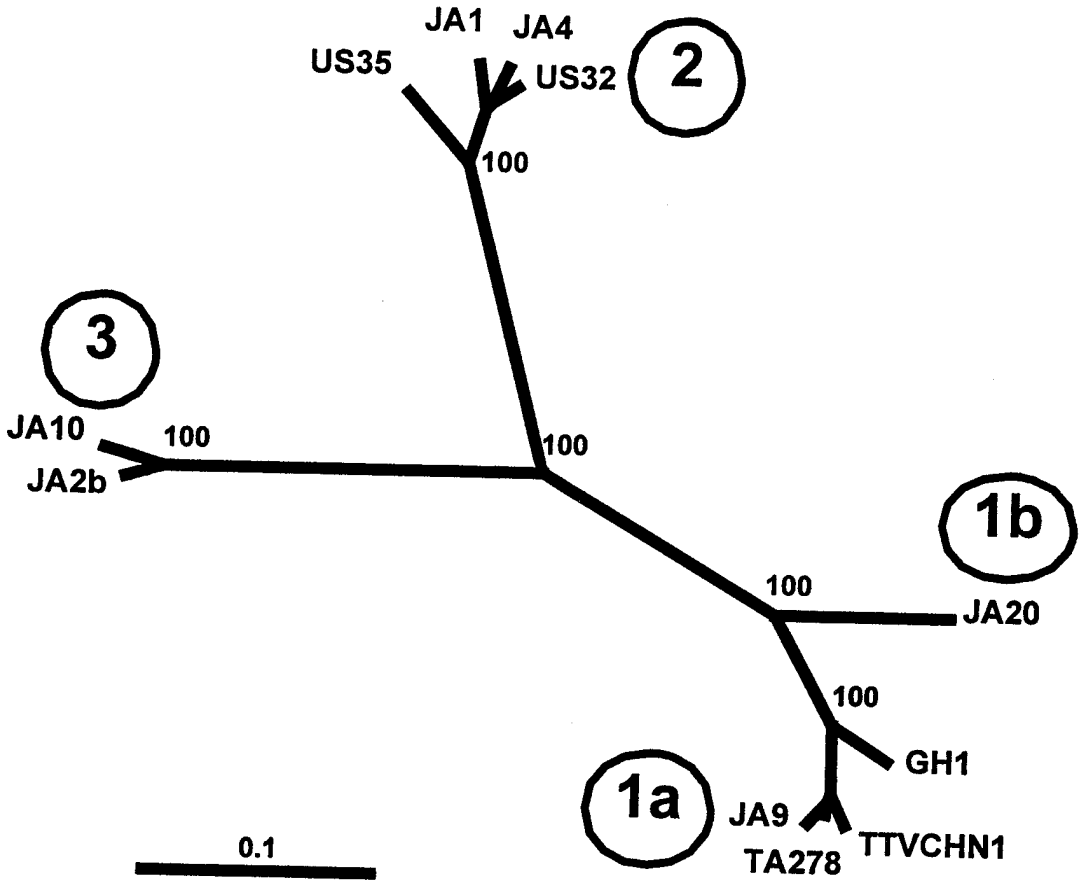
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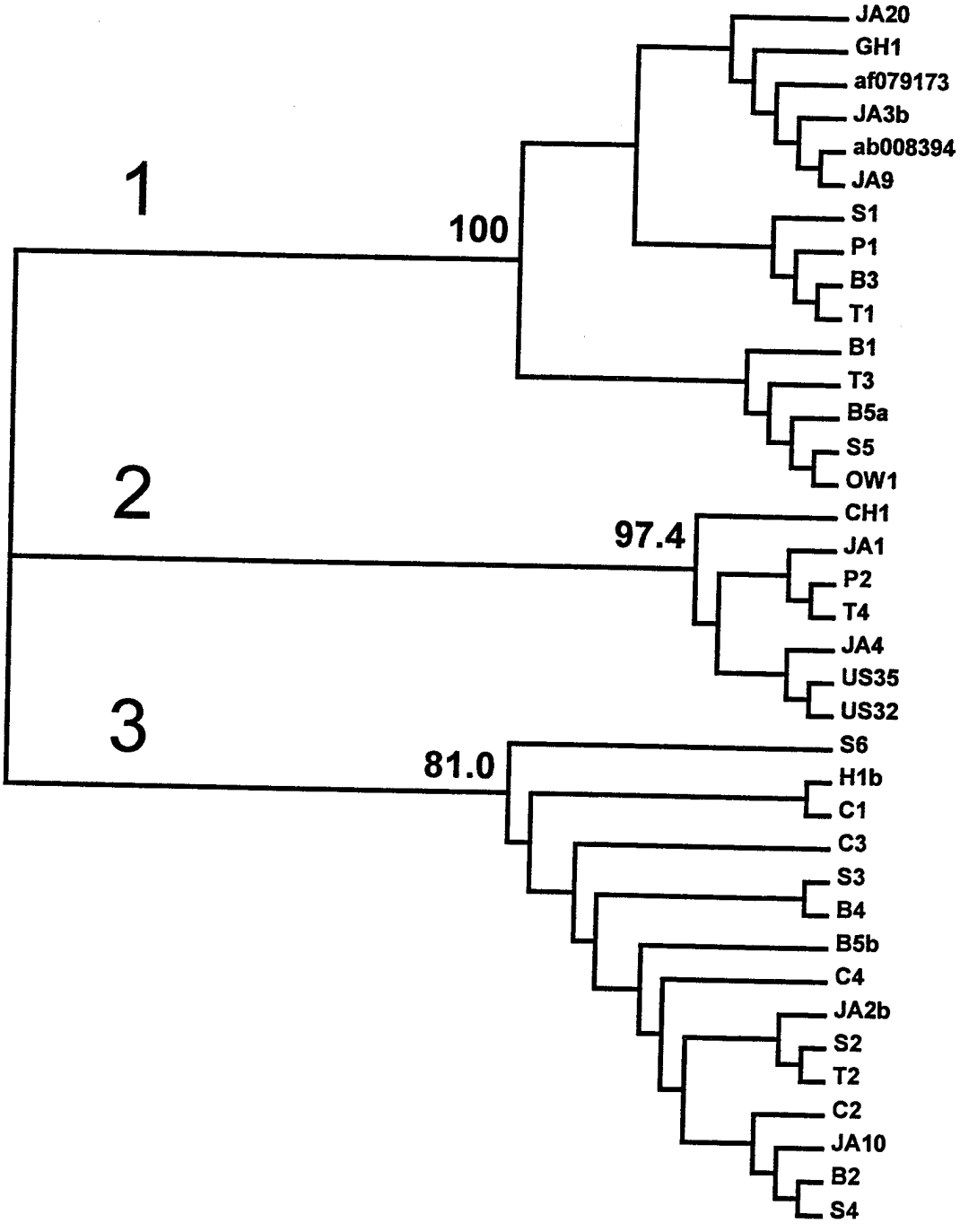
Figure 7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B4
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T2
C2
JA10
B2
S4

专利名称(译)	利用tt病毒的方法		
公开(公告)号	EP1220946A2	公开(公告)日	2002-07-10
申请号	EP2000907172	申请日	2000-02-04
[标]申请(专利权)人(译)	雅培公司		
申请(专利权)人(译)	亚培		
当前申请(专利权)人(译)	亚培		
[标]发明人	LEARY THOMAS P SIMONS JOHN N ERKER JAMES C CHALMERS MICHELE L BIRKENMEYER LARRY G MUERHOFF A SCOTT PILOT MATIAS TAMI J DESAI SURESH M MUSHAHWAR ISA K		
发明人	LEARY, THOMAS, P. SIMONS, JOHN, N. ERKER, JAMES, C. CHALMERS, MICHELE, L. BIRKENMEYER, LARRY, G. MUERHOFF, A., SCOTT PILOT-MATIAS, TAMI, J. DESAI, SURESH, M. MUSHAHWAR, ISA, K.		
IPC分类号	G01N33/53 C12N1/15 C12N1/19 C12N5/10 C12N15/09 C12Q1/68 C12Q1/70 G01N33/566 C12N15/86		
CPC分类号	C12Q1/701 Y10S977/804		
优先权	09/245248 1999-02-05 US		
外部链接	Espacenet		

摘要(译)

本发明涉及用于检测测试样品中TTV的核酸寡聚物引物或探针。还提供了利用这些引物和探针的测定法，以及含有这些寡聚物引物和/或探针的测试试剂盒。此外，本发明包括TTV核苷酸序列作为核酸载体的用途以及用于确定个体之间传递的标志物及其途径。另外，本发明包括在组织或器官的异种移植之前检测TTV感染的方法。